

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> MetA

<130> M/43127

<140>

<141>

<160> 58

<210> 1

<211> 1104

<212> DNA

<213> Corynebacterium diphtheriae

<220>

<221> CDS

<222> (1)..(1101)

<223> RDI00386

<400> 1

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tac acc gaa gcc gga gcg acg ctt cac gac gta acc atc gcc tac caa	96
Tyr Thr Glu Ala Gly Ala Thr Leu His Asp Val Thr Ile Ala Tyr Gln	
20 25 30	

gca tgg ggc cac tac acc ggc acc aat ctc atc gtt ctc gaa cat gcc	144
Ala Trp Gly His Tyr Thr Gly Thr Asn Leu Ile Val Leu Glu His Ala	
35 40 45	

ctg acc ggc gac tct aac gct att tca tgg tgg gac gga ctg att ggc	192
Leu Thr Gly Asp Ser Asn Ala Ile Ser Trp Trp Asp Gly Leu Ile Gly	
50 55 60	

cct ggc aaa gca ctc gac acc aac cgc tac tgc atc cta tgc acc aac	240
Pro Gly Lys Ala Leu Asp Thr Asn Arg Tyr Cys Ile Leu Cys Thr Asn	
65 70 75 80	

gtg ctc gga gga tgc aaa gga tcc acc gga ccg agc agt cca cac cca	288
Val Leu Gly Gly Cys Lys Gly Ser Thr Gly Pro Ser Ser Pro His Pro	
85 90 95	

gac gga aaa cca tgg gga tcc aga ttt cca gcc ctt tca atc cgt gac	336
Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Ala Leu Ser Ile Arg Asp	
100 105 110	

ctt gtc aat gcc gaa aaa caa ctt ttc gac cac ctc ggc atc aat aaa	384
Leu Val Asn Ala Glu Lys Gln Leu Phe Asp His Leu Gly Ile Asn Lys	
115 120 125	

att cac gca atc atc ggc gga tcc atg gga ggc gca cgc acc ctc gaa	432
Ile His Ala Ile Ile Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu	
130 135 140	

tgg gct gca ctc cac cca cac atg atg acg act gga ttc gtc ata gca	480
Trp Ala Ala Leu His Pro His Met Met Thr Thr Gly Phe Val Ile Ala	
145 150 155 160	

gtc tca gca cgc gca agc gct tgg caa atc ggt att caa act gca caa	528
Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Thr Ala Gln	

165	170	175	
atc agc gcc ata gaa ctc gac ccc cac tgg aac ggc ggc gat tac tac Ile Ser Ala Ile Glu Leu Asp Pro His Trp Asn Gly Gly Asp Tyr Tyr 180	185	190	576
agc ggt cac gca cca tgg gaa gga atc gcc gcc gct cgc cgcc atc gcc Ser Gly His Ala Pro Trp Glu Gly Ile Ala Ala Ala Arg Arg Ile Ala 195	200	205	624
cac ctc acc tat cgc ggc gaa cta gaa ata gac gaa cga ttc ggc act His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg Phe Gly Thr 210	215	220	672
tcc gca caa cac ggt gaa aac cca ctc ggc ccc ttc cga gat cca cat Ser Ala Gln His Gly Glu Asn Pro Leu Gly Pro Phe Arg Asp Pro His 225	230	235	720
caa cgt ttt gcg gtc acg arg tac ctc caa cac caa ggc atc aaa ctc Gln Arg Phe Ala Val Thr Ser Tyr Leu Gln His Gln Gly Ile Lys Leu 245	250	255	768
gct caa cga ttc gat gca ggt agt tac gtc gtg ctt acc gaa gcc ctc Ala Gln Arg Phe Asp Ala Gly Ser Tyr Val Val Leu Thr Glu Ala Leu 260	265	270	816
aat cgt cat gac atc gga cgc ggc cga ggc gga ctc aac aaa gcc ctc Asn Arg His Asp Ile Gly Arg Gly Arg Gly Leu Asn Lys Ala Leu 275	280	285	864
agc gca atc aca gtc ccc atc atg att gct ggc gtt gat acc gat att Ser Ala Ile Thr Val Pro Ile Met Ile Ala Gly Val Asp Thr Asp Ile 290	295	300	912
ctc tac ccc tat cac cag caa gaa cac cta tca cga aat cta ggc aac Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn Leu Gly Asn 305	310	315	960
cta ctc gct atg gca aaa atc agc tca cca gta ggc cac gac gct ttc Leu Leu Ala Met Ala Lys Ile Ser Ser Pro Val Gly His Asp Ala Phe 325	330	335	1008
ctc aca gaa ttc cga caa atg gag cga atc cta aga cat ttc atg gag Leu Thr Glu Phe Arg Gln Met Glu Arg Ile Leu Arg His Phe Met Glu 340	345	350	1056
ctt tcg gaa gga atc gac gat tcc ttc cga acc aaa cta gag cgc Leu Ser Glu Gly Ile Asp Asp Ser Phe Arg Thr Lys Leu Glu Arg 355	360	365	1101
tga			1104

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<212> PRT
<213> Corynebacterium diphtheriae

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Tyr Thr Glu Ala Gly Ala Thr Leu His Asp Val Thr Ile Ala Tyr Gln 20	25	30	
Ala Trp Gly His Tyr Thr Gly Thr Asn Leu Ile Val Leu Glu His Ala 35	40	45	

Leu Thr Gly Asp Ser Asn Ala Ile Ser Trp Trp Asp Gly Leu Ile Gly
 50 55 60

Pro Gly Lys Ala Leu Asp Thr Asn Arg Tyr Cys Ile Leu Cys Thr Asn
 65 70 75 80

Val Leu Gly Gly Cys Lys Gly Ser Thr Gly Pro Ser Ser Pro His Pro
 85 90 95

Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Ala Leu Ser Ile Arg Asp
 100 105 110

Leu Val Asn Ala Glu Lys Gln Leu Phe Asp His Leu Gly Ile Asn Lys
 115 120 125

Ile His Ala Ile Ile Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu
 130 135 140

Trp Ala Ala Leu His Pro His Met Met Thr Thr Gly Phe Val Ile Ala
 145 150 155 160

Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Thr Ala Gln
 165 170 175

Ile Ser Ala Ile Glu Leu Asp Pro His Trp Asn Gly Gly Asp Tyr Tyr
 180 185 190

Ser Gly His Ala Pro Trp Glu Gly Ile Ala Ala Ala Arg Arg Ile Ala
 195 200 205

His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg Phe Gly Thr
 210 215 220

Ser Ala Gln His Gly Glu Asn Pro Leu Gly Pro Phe Arg Asp Pro His
 225 230 235 240

Gln Arg Phe Ala Val Thr Ser Tyr Leu Gln His Gln Gly Ile Lys Leu
 245 250 255

Ala Gln Arg Phe Asp Ala Gly Ser Tyr Val Val Leu Thr Glu Ala Leu
 260 265 270

Asn Arg His Asp Ile Gly Arg Gly Arg Gly Leu Asn Lys Ala Leu
 275 280 285

Ser Ala Ile Thr Val Pro Ile Met Ile Ala Gly Val Asp Thr Asp Ile
 290 295 300

Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn Leu Gly Asn
 305 310 315 320

Leu Leu Ala Met Ala Lys Ile Ser Ser Pro Val Gly His Asp Ala Phe
 325 330 335

Leu Thr Glu Phe Arg Gln Met Glu Arg Ile Leu Arg His Phe Met Glu
 340 345 350

Leu Ser Glu Gly Ile Asp Asp Ser Phe Arg Thr Lys Leu Glu Arg
 355 360 365

<210> 3
 <211> 1149
 <212> DNA
 <213> Mycobacterium leprae

<220>
<221> CDS
<222> (1)...(1146)
<223> RML02951

<220>
<221> unsure

<222> 224 .. 224
<223> All occurrences of n indicate any nucleotide

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1 5 10 15

gtc ggc ttg gtc gac atc ggc tca ctt acc acc gaa agc ggt gcc gtc 96
Val Gly Leu Val Asp Ile Gly Ser Leu Thr Thr Glu Ser Gly Ala Val
20 25 30

atc gac gat gtc tgc atc gcc gtt cag cgc tgg ggg gaa ttg tcg ccc 144
Ile Asp Asp Val Cys Ile Ala Val Gln Arg Trp Gly Glu Leu Ser Pro
35 40 45

acg cga gac aac gta gtg atg gta ctg cat gca ctc acc ggt gac tcg 192
Thr Arg Asp Asn Val Val Met Val Leu His Ala Leu Thr Gly Asp Ser
50 55 60

cac atc acc ggg ccc gcc gga ccg gga cat cnc aca ccc ggc tgg tgg 240
His Ile Thr Gly Pro Ala Gly Pro Gly His Xaa Thr Pro Gly Trp Trp
65 70 75 80

gac tgg ata gct gga ccg ggt gca cca atc gac acc aac cgc tgg tgc 288
Asp Trp Ile Ala Gly Pro Gly Ala Pro Ile Asp Thr Asn Arg Trp Cys
85 90 95

gcg ata gcc acc aac gtg ctg ggc ggt tgc cgt ggc tcc acc ggc cct 336
Ala Ile Ala Thr Asn Val Leu Gly Gly Cys Arg Gly Ser Thr Gly Pro
100 105 110

agt tcg ctt gcc cgc gac gga aag cct tgg ggt tca aga ttt ccg ctg 384
Ser Ser Leu Ala Arg Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Leu
115 120 125

ata tct ata cgc gac cag gta gag gca gat atc gct gca ctg gcc gcc 432
Ile Ser Ile Arg Asp Gln Val Glu Ala Asp Ile Ala Ala Leu Ala Ala
130 135 140

atg gga att aca aag gtt gcc gcc gtc gtt gga gga tct atg ggc ggg 480
Met Gly Ile Thr Lys Val Ala Ala Val Val Gly Gly Ser Met Gly Gly
145 150 155 160

gcg cgt gca ctg gaa tgg atc atc ggc cac ccg gac caa gtc cgg gcc 528
Ala Arg Ala Leu Glu Trp Ile Ile Gly His Pro Asp Gln Val Arg Ala
165 170 175

ggg ctg ttg ctg gcg gtc ggt gtg cgc gcc acc gcc gac cag atc ggc 576
Gly Leu Leu Leu Ala Val Gly Val Arg Ala Thr Ala Asp Gln Ile Gly
180 185 190

acc caa acc acc caa atc gca gcc atc aag aca gac ccg aac tgg caa 624
Thr Gln Thr Gln Ile Ala Ala Ile Lys Thr Asp Pro Asn Trp Gln
195 200 205

ggc ggt gac tac tac gag aca ggg agg gca cca gag aac ggc ttg aca 672
Gly Gly Asp Tyr Tyr Glu Thr Gly Arg Ala Pro Glu Asn Gly Leu Thr

210	215	220	
att gcc cgc cgc ttc gcc cac ctg acc tac cgc agc gag gtc gag ctc Ile Ala Arg Arg Phe Ala His Leu Thr Tyr Arg Ser Glu Val Glu Leu 225	230	235	720 240
gac acc cg ^g ttt gcc aac aac aac caa ggc aat gag gac ccg gcg acg Asp Thr Arg Phe Ala Asn Asn Asn Gln Gly Asn Glu Asp Pro Ala Thr 245		250	768 255
ggc ggg cgt tac gca gtg cag agt tac cta gag cac cag ggt gac aag Gly Gly Arg Tyr Ala Val Gln Ser Tyr Leu Glu His Gln Gly Asp Lys 260	265		816 270
cta ttg gcc cgc ttt gac gca ggc agc tac gtg gtc ttg acc gaa acg Leu Leu Ala Arg Phe Asp Ala Gly Ser Tyr Val Val Leu Thr Glu Thr 275	280	285	864
ctg aac agc cac gac gtt ggc cg ^g ggc cgc gga ggg atc ggt aca gcg Leu Asn Ser His Asp Val Gly Arg Gly Arg Gly Gly Ile Gly Thr Ala 290	295	300	912
ctg cgc ggg tgc cc ^g gta cc ^g gtg gtg ggt ggc att acc tcg gat Leu Arg Gly Cys Pro Val Pro Val Val Gly Gly Ile Thr Ser Asp 305	310	315	960 320
cg ^g ctc tac cca ctg cgc ttg cag cag gag ctg gcc gag atg ctg ccg Arg Leu Tyr Pro Leu Arg Leu Gln Gln Glu Leu Ala Glu Met Leu Pro 325	330	335	1008
ggc tgc acc ggg ctg cag gtt gta gac tcc acc tac ggg cac gac ggc Gly Cys Thr Gly Leu Gln Val Val Asp Ser Thr Tyr Gly His Asp Gly 340	345	350	1056
ttc ctg gtg gaa tcc gag gcc gtc ggc aaa ttg atc cgtcaa acc ctc Phe Leu Val Glu Ser Glu Ala Val Gly Lys Leu Ile Arg Gln Thr Leu 355	360	365	1104
gaa ttg gcc gac gtg ggt tcc aag gaa gac gcg tgc tgc caa Glu Leu Ala Asp Val Gly Ser Lys Glu Asp Ala Cys Ser Gln 370	375	380	1146
tga			1149

<210> 4
<211> 382
<212> PRT
<213> *Mycobacterium leprae*

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<220>
<221> unsure
<222> 75 .. 75
<223> All occurrences of Xaa indicate any amino acid
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Val Gly Leu Val Asp Ile Gly Ser Leu Thr Thr Glu Ser Gly Ala Val
20 25 30

Ile Asp Asp Val Cys Ile Ala Val Gln Arg Trp Gly Glu Leu Ser Pro
35 40 45

Thr Arg Asp Asn Val Val Met Val Leu His Ala Leu Thr Gly Asp Ser

50	55	60
His Ile Thr Gly Pro Ala Gly Pro Gly His Xaa	70	75
65		80
Asp Trp Ile Ala Gly Pro Gly Ala Pro Ile Asp	85	90
Thr Asn Arg Trp Cys		95
Ala Ile Ala Thr Asn Val Leu Gly Gly Cys Arg	100	105
Gly Ser Thr Gly Pro		110
Ser Ser Leu Ala Arg Asp Gly Lys Pro Trp Gly Ser	115	120
Arg Phe Pro Leu		125
Ile Ser Ile Arg Asp Gln Val Glu Ala Asp Ile	130	135
Ala Ala Leu Ala Ala		140
Met Gly Ile Thr Lys Val Ala Ala Val Val Gly	145	150
Gly Ser Met Gly Gly		155 160
Ala Arg Ala Leu Glu Trp Ile Ile Gly His Pro Asp	165	170
Gln Val Arg Ala		175
Gly Leu Leu Leu Ala Val Gly Val Arg Ala Thr	180	185
Ala Asp Gln Ile Gly		190
Thr Gln Thr Thr Gln Ile Ala Ala Ile Lys Thr Asp	195	200
Pro Asn Trp Gln		205
Gly Gly Asp Tyr Tyr Glu Thr Gly Arg Ala Pro	210	215
Glu Asn Gly Leu Thr		220
Ile Ala Arg Arg Phe Ala His Leu Thr Tyr Arg	225	230
Ser Glu Val Glu Leu		235 240
Asp Thr Arg Phe Ala Asn Asn Gln Gly Asn Glu Asp	245	250
Pro Ala Thr		255
Gly Gly Arg Tyr Ala Val Gln Ser Tyr Leu Glu His	260	265
Gln Gly Asp Lys		270
Leu Leu Ala Arg Phe Asp Ala Gly Ser Tyr Val Val	275	280
Leu Thr Glu Thr		285
Leu Asn Ser His Asp Val Gly Arg Gly Arg Gly	290	295
Gly Ile Gly Thr Ala		300
Leu Arg Gly Cys Pro Val Pro Val Val Val Gly	305	310
Gly Ile Thr Ser Asp		315 320
Arg Leu Tyr Pro Leu Arg Leu Gln Gln Glu Leu Ala	325	330
Glu Met Leu Pro		335
Gly Cys Thr Gly Leu Gln Val Val Asp Ser Thr Tyr	340	345
Gly His Asp Gly		350
Phe Leu Val Glu Ser Glu Ala Val Gly Lys Leu Ile Arg	355	360
Gln Thr Leu		365
Glu Leu Ala Asp Val Gly Ser Lys Glu Asp Ala Cys	370	375
Ser Gln		380

<210> 5
<211> 1140
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<221> CDS
<222> (1)..(1137)
<223> RMTB03565

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ctg tta tcc cgg ttc gac gcc ggc agc tac gtg att ctc acc gag gcg Leu Leu Ser Arg Phe Asp Ala Gly Ser Tyr Val Ile Leu Thr Glu Ala 275 280 285	864
ctc aac agc cac gac gtc ggc cgc ggc ggc ggg gtc tcc gcg gct Leu Asn Ser His Asp Val Gly Arg Gly Arg Gly Val Ser Ala Ala 290 295 300	912
ctg cgc gcc tgc ccg gtg ccg gtg gtg gtg ggc ggc atc acc tcc gac Leu Arg Ala Cys Pro Val Pro Val Val Gly Gly Ile Thr Ser Asp 305 310 315 320	960
cgg ctc tac ccg ctg cgc ctg cag cag gag ctg gcc gac ctg ctg ccg Arg Leu Tyr Pro Leu Arg Leu Gln Gln Glu Leu Ala Asp Leu Leu Pro 325 330 335	1008
ggc tgc gcc ggg ctg cga gtc gag tcg gtc tac gga cac gac ggc Gly Cys Ala Gly Leu Arg Val Val Glu Ser Val Tyr Gly His Asp Gly 340 345 350	1056
ttc ctg gtg gaa acc gag gcc gtg ggc gaa ttg atc cgc cag aca ctg Phe Leu Val Glu Thr Glu Ala Val Gly Glu Leu Ile Arg Gln Thr Leu 355 360 365	1104
gga ttg gct gat cgt gaa ggc gcg tgt cgg cgg tga Gly Leu Ala Asp Arg Glu Gly Ala Cys Arg Arg 370 375	1140

<210> 6
<211> 379
<212> PRT
<213> Mycobacterium tuberculosis

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Ile Asp Asp Val Cys Ile Ala Val Gln Arg Trp Gly Lys Leu Ser Pro 35 40 45
Ala Arg Asp Asn Val Val Val Leu His Ala Leu Thr Gly Asp Ser 50 55 60
His Ile Thr Gly Pro Ala Gly Pro Gly His Pro Thr Pro Gly Trp Trp 65 70 75 80
Asp Gly Val Ala Gly Pro Ser Ala Pro Ile Asp Thr Thr Arg Trp Cys 85 90 95
Ala Val Ala Thr Asn Val Leu Gly Gly Cys Arg Gly Ser Thr Gly Pro 100 105 110
Ser Ser Leu Ala Arg Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Leu

115	120	125
Ile Ser Ile Arg Asp Gln Val	Gln Ala Asp Val	Ala Ala Leu Ala Ala
130	135	140
Leu Gly Ile Thr Glu Val Ala Ala Val Val	Gly Gly Ser Met Gly Gly	
145	150	155 160
Ala Arg Ala Leu Glu Trp Val Val	Gly Tyr Pro Asp Arg Val	Arg Ala
165	170	175
Gly Leu Leu Leu Ala Val Gly Ala Arg Ala Thr Ala Asp Gln	Ile Gly	
180	185	190
Thr Gln Thr Thr Gln Ile Ala Ala	Ile Lys Ala Asp Pro Asp Trp	Gln
195	200	205
Ser Gly Asp Tyr His Glu Thr Gly Arg Ala Pro Asp Ala Gly Leu Arg		
210	215	220
Leu Ala Arg Arg Phe Ala His Leu Thr Tyr Arg Gly Glu Ile Glu Leu		
225	230	235 240
Asp Thr Arg Phe Ala Asn His Asn Gln Gly Asn Glu Asp Pro Thr Ala		
245	250	255
Gly Gly Arg Tyr Ala Val Gln Ser Tyr Leu Glu His Gln Gly Asp Lys		
260	265	270
Leu Leu Ser Arg Phe Asp Ala Gly Ser Tyr Val Ile Leu Thr Glu Ala		
275	280	285
Leu Asn Ser His Asp Val Gly Arg Gly Arg Gly Val Ser Ala Ala		
290	295	300
Leu Arg Ala Cys Pro Val Pro Val Val Val Gly Gly Ile Thr Ser Asp		
305	310	315 320
Arg Leu Tyr Pro Leu Arg Leu Gln Gln Glu Leu Ala Asp Leu Leu Pro		
325	330	335
Gly Cys Ala Gly Leu Arg Val Val Glu Ser Val Tyr Gly His Asp Gly		
340	345	350
Phe Leu Val Glu Thr Glu Ala Val Gly Glu Leu Ile Arg Gln Thr Leu		
355	360	365
Gly Leu Ala Asp Arg Glu Gly Ala Cys Arg Arg		
370	375	

<210> 7
 <211> 972
 <212> DNA
 <213> Chlorobium tepidum

<220>
 <221> CDS
 <222> (1)...(969)
 <223> RCL01447

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 1 5 10 15
 aac gtg att ctg gtc tgc cac gcg ctg acc ggc aac gcc gac gcc gac 96

Asn Val Ile Leu Val Cys His Ala Leu Thr Gly Asn Ala Asp Ala Asp			
20	25	30	
agc tgg tgg tgc ggc atg ttc ggt gag gga cgg gcg ttc gac gag act			144
Ser Trp Trp Cys Gly Met Phe Gly Glu Gly Arg Ala Phe Asp Glu Thr			
35	40	45	
cgg gac ttc atc gta tgc agc aac gtg ctt gga agc tgc tac gga acg			192
Arg Asp Phe Ile Val Cys Ser Asn Val Leu Gly Ser Cys Tyr Gly Thr			
50	55	60	
acc ggg ccg atg tcg gtg aat ccg ctg agt ggc agg cac tac ggt ccc			240
Thr Gly Pro Met Ser Val Asn Pro Leu Ser Gly Arg His Tyr Gly Pro			
65	70	75	80
gat ttt ccg cgc att acc att cgc gac atg gtg aat gtt cag cga tta			288
Asp Phe Pro Arg Ile Thr Ile Arg Asp Met Val Asn Val Gln Arg Leu			
85	90	95	
ttg ctt cgt tcg ctc ggc atc gac cgg atc cgg ctc atc gtt ggt gca			336
Leu Leu Arg Ser Leu Gly Ile Asp Arg Ile Arg Leu Ile Val Gly Ala			
100	105	110	
tcg ctt ggc ggg atg cag gtg ctc gaa tgg ggc gca atg tat ccc gaa			384
Ser Leu Gly Gly Met Gln Val Leu Glu Trp Gly Ala Met Tyr Pro Glu			
115	120	125	
atg gcc ggg gcg ctg atg ccg atg ggc gtt tcg ggt cgt cat tcg gcg			432
Met Ala Gly Ala Leu Met Pro Met Gly Val Ser Gly Arg His Ser Ala			
130	135	140	
tgg tgc atc gcg cag agc gag gcg cag cgg cag gct atc gcc gcc gat			480
Trp Cys Ile Ala Gln Ser Glu Ala Gln Arg Gln Ala Ile Ala Ala Asp			
145	150	155	160
gcg gag tgg caa gat ggc tgg tat gat ccg gag gtg cag cca cgc aaa			528
Ala Glu Trp Gln Asp Gly Trp Tyr Asp Pro Glu Val Gln Pro Arg Lys			
165	170	175	
gga ctt gcc gcc gcg cgg atg atg gcg atg tgc acc tac cgc tgc ttc			576
Gly Leu Ala Ala Arg Met Met Ala Met Cys Thr Tyr Arg Cys Phe			
180	185	190	
gag aac tac cag caa cgc ttt ggc cgc aag cag cgc gag gac ggc ttg			624
Glu Asn Tyr Gln Gln Arg Phe Gly Arg Lys Gln Arg Glu Asp Gly Leu			
195	200	205	
ttc gaa gcc gaa agc tac gtg cgt cac cag ggc gac aag ctg gtt ggg			672
Phe Glu Ala Glu Ser Tyr Val Arg His Gln Gly Asp Lys Leu Val Gly			
210	215	220	
cgc ttt gat gca aac acc tat atc acg ctc acc aga gcg atg gac atg			720
Arg Phe Asp Ala Asn Thr Tyr Ile Thr Leu Thr Arg Ala Met Asp Met			
225	230	235	240
cac gac ctc ggg cgc gga cgc gac tcc tac gaa gcg gcg ctc gga gcg			768
His Asp Leu Gly Arg Gly Arg Asp Ser Tyr Glu Ala Ala Leu Gly Ala			
245.	250	255	
ctg aag atg ccg gtc gag att ctc tcc atc gac tcg gac gtg ctc tat			816
Leu Lys Met Pro Val Glu Ile Leu Ser Ile Asp Ser Asp Val Leu Tyr			
260	265	270	
ccc agg cag gag cag gag gaa ctt gcc cgc ctc att ccc ggc tca cgc			864
Pro Arg Gln Glu Gln Glu Glu Leu Ala Arg Leu Ile Pro Gly Ser Arg			
275	280	285	

ctg ctt ttc ctt gac gaa ccc tat ggc cac gac gcc ttt ctt atc gac	912
Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp	
290 295 300	
acc gag acc gtc agc cgc atg gtc tgc gag ttc aag agg cag ttg ata	960
Thr Glu Thr Val Ser Arg Met Val Cys Glu Phe Lys Arg Gln Leu Ile	
305 310 315 320	
gtt gac aat tga	972
Val Asp Asn	

<210> 8
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<212> PRT
<213> Chlorobium tepidum

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Ser Trp Trp Cys Gly Met Phe Gly Glu Gly Arg Ala Phe Asp Glu Thr	
35 40 45	
Arg Asp Phe Ile Val Cys Ser Asn Val Leu Gly Ser Cys Tyr Gly Thr	
50 55 60	
Thr Gly Pro Met Ser Val Asn Pro Leu Ser Gly Arg His Tyr Gly Pro	
65 70 75 80	
Asp Phe Pro Arg Ile Thr Ile Arg Asp Met Val Asn Val Gln Arg Leu	
85 90 95	
Leu Leu Arg Ser Leu Gly Ile Asp Arg Ile Arg Leu Ile Val Gly Ala	
100 105 110	
Ser Leu Gly Gly Met Gln Val Leu Glu Trp Gly Ala Met Tyr Pro Glu	
115 120 125	
Met Ala Gly Ala Leu Met Pro Met Gly Val Ser Gly Arg His Ser Ala	
130 135 140	
Trp Cys Ile Ala Gln Ser Glu Ala Gln Arg Gln Ala Ile Ala Ala Asp	
145 150 155 160	
Ala Glu Trp Gln Asp Gly Trp Tyr Asp Pro Glu Val Gln Pro Arg Lys	
165 170 175	
Gly Leu Ala Ala Ala Arg Met Met Ala Met Cys Thr Tyr Arg Cys Phe	
180 185 190	
Glu Asn Tyr Gln Gln Arg Phe Gly Arg Lys Gln Arg Glu Asp Gly Leu	
195 200 205	
Phe Glu Ala Glu Ser Tyr Val Arg His Gln Gly Asp Lys Leu Val Gly	
210 215 220	
Arg Phe Asp Ala Asn Thr Tyr Ile Thr Leu Thr Arg Ala Met Asp Met	
225 230 235 240	
His Asp Leu Gly Arg Gly Arg Asp Ser Tyr Glu Ala Ala Leu Gly Ala	
245 250 255	

Leu Lys Met Pro Val Glu Ile Leu Ser Ile Asp Ser Asp Val Leu Tyr
 260 265 270

Pro Arg Gln Glu Gln Glu Glu Leu Ala Arg Leu Ile Pro Gly Ser Arg
 275 280 285

Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp
 290 295 300

Thr Glu Thr Val Ser Arg Met Val Cys Glu Phe Lys Arg Gln Leu Ile
 305 310 315 320

Val Asp Asn

<210> 9
 <211> 1149
 <212> DNA
 <213> Caulobacter crescentus

<220>
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 <222> (1)..(1146)
 <223> RCO00727

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 1 5 10 15

ttt cct gcg aat gaa cct ctg cgg ctg gac tcc gga ggc gtc atc gaa 96
 Phe Pro Ala Asn Glu Pro Leu Arg Leu Asp Ser Gly Gly Val Ile Glu
 20 25 30

ggc ctg gaa atc gcc tac cag acc tac ggc cag ctg aac gcg gac aag 144
 Gly Leu Glu Ile Ala Tyr Gln Thr Tyr Gly Gln Leu Asn Ala Asp Lys
 35 40 45

tcc aac gcc gtc ctg atc tgc cac gcc ctg acg ggc gac cag cat gtg 192
 Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val
 50 55 60

gcc tcg ccc cac ccc acc acc ggc aag ccc ggc tgg tgg caa cgc ctt 240
 Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu
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gtt ggt ccc ggt aag ccg ctg gat ccc gcg cgg cac ttc atc atc tgc 288
 Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys
 85 90 95

tcg aac gtg atc ggc ggc tgc atg ggc tcg acg ggc ccg gcc tcg atc 336
 Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile
 100 105 110

aat ccg gcc acg ggc aag acc tat ggc ctg tcg ttc cca gtc atc acc 384
 Asn Pro Ala Thr Gly Lys Thr Tyr Gly Leu Ser Phe Pro Val Ile Thr
 115 120 125

atc gcc gat atg gtg cgg gcc cag gcc atg ctg gtc tct gcg ctc ggg 432
 Ile Ala Asp Met Val Arg Ala Gln Ala Met Leu Val Ser Ala Leu Gly
 130 135 140

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 Val Glu Thr Leu Phe Ala Val Val Gly Gly Ser Met Gly Gly Met Gln
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Val Gln Gln Trp Ala Val Asp Tyr Pro Glu Arg Met Phe Ser Ala Val	
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Val Leu Ala Ser Ala Ser Arg His Ser Ala Gln Asn Ile Ala Phe His	
180 185 190	
gag gtg ggc cgc cag gcg atc atg gcc gat ccc gac tgg cgc ggc ggc	624
Glu Val Gly Arg Gln Ala Ile Met Ala Asp Pro Asp Trp Arg Gly Gly	
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gcc tat gcc gag cac ggc gtg cgg ccc gag aag ggc ctg gcc gtg gcg	672
Ala Tyr Ala Glu His Gly Val Arg Pro Glu Lys Gly Leu Ala Val Ala	
210 215 220	
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Arg Met Ala Ala His Ile Thr Tyr Leu Ser Glu Pro Ala Leu Gln Arg	
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Lys Phe Gly Arg Glu Leu Gln Arg Asp Gly Leu Ser Trp Gly Phe Asp	
245 250 255	
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Ala Asp Phe Gln Val Glu Ser Tyr Leu Arg His Gln Gly Ser Ser Phe	
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gtc gac cgg ttc gac gcc aac agc tat ctc tac atc acc cgg gcc atg	864
Val Asp Arg Phe Asp Ala Asn Ser Tyr Leu Tyr Ile Thr Arg Ala Met	
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gac tat ttc gac atc gcc gcc agc cat ggc ggg gtg ctg gcc aag gcg	912
Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala	
290 295 300	
ttc acc cga gcg cgg aat gtc cgc ttc tgc gtg ctg agc ttc tcc agc	960
Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser	
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Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu	
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acc gcc gcc ggg gcc cgc gcg gcc ttc gcc gag atc gag agc gac aag	1056
Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys	
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Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu	
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gaa ggc ttc ctg gcc tcg gcc gaa cgc gat cgg ggg ctg gtt	1146
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<213> Caulobacter crescentus

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Ser	Asn	Ala	Val
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Thr	Thr	Gly	Lys
Pro	Gly	Lys	Pro
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Arg	His	Arg	Phe
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Ser	Asn	Val	Ile
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Met	Gly	Ser	Thr
Tyr	Gly	Pro	Ala
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Ser	Pro	Ala	Thr
Asn	Asn	Ala	Thr
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Asp	Pro	Asp	Pro
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Val	Asp	Met	Ile
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200	205	210	215
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205	210	215	220
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Val	Asp	Met	Ile
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215	220	225	230
Met	Val	Asp	Ile
Val	Asp	Met	Ile
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Asp	Asp	Asp	Asp
225	230	235	240
Met	Val	Asp	Ile
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Asp	Asp	Asp	Asp
235	240	245	250
Met	Val	Asp	Ile
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255	260	265	270
Met	Val	Asp	Ile
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265	270	275	280
Met	Val	Asp	Ile
Val	Asp	Met	Ile
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275	280	285	290
Met	Val	Asp	Ile
Val	Asp	Met	Ile
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Asp	Asp	Asp	Asp
285	290	295	300
Met	Val	Asp	Ile
Val	Asp	Met	Ile
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Gly	Gly	Gly	Gly
Asp	Asp	Asp	Asp
295	300	305	310
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Asp	Asp	Asp	Asp
315	320	325	330
Met	Val	Asp	Ile
Val	Asp	Met	Ile
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425	430	435	440
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435	440	445	450
Met	Val	Asp	Ile
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445	450	455	460
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Val	Asp	Met	Ile
450	455	460	
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455	460	465	470
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Val	Asp	Met	Ile
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465	470	475	480
Met	Val	Asp	Ile
Val	Asp	Met	Ile
470	475	480	
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Asp	Asp	Asp	Asp
475	480	485	490
Met	Val	Asp	Ile
Val	Asp	Met	Ile
480	485	490	
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Asp	Asp	Asp	Asp
485	490	495	500
Met	Val	Asp	Ile
Val	Asp	Met	Ile
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Gly	Gly	Gly	Gly
Asp	Asp	Asp	Asp
495	500	505	510
Met	Val	Asp	Ile
Val	Asp	Met	Ile
500	505	510	
Gly	Gly	Gly	Gly
Asp	Asp	Asp	Asp
505	510	515	520
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Gly	Gly	Gly	Gly
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Val	Asp	Met	Ile
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525	530	535	540
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Val	Asp	Met	Ile
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Gly	Gly	Gly	Gly
Asp	Asp	Asp	Asp
535	540	545	550
Met	Val	Asp	Ile
Val	Asp	Met	Ile
540	545	550	
Gly	Gly	Gly	Gly
Asp	Asp	Asp	Asp
545	550	555	560
Met	Val	Asp	Ile
Val	Asp	Met	Ile
550	555	560	
Gly	Gly	Gly	Gly
Asp	Asp	Asp	Asp
555	560	565	570
Met	Val	Asp	Ile
Val	Asp	Met	Ile
560	565	570	
Gly	Gly	Gly	Gly
Asp	Asp	Asp	Asp
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Met			

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<223> RNG00132

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gat ctg atg att gaa acc tac ggc gag ctg aat gct gaa aaa aac aat 144
 Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
 35 40 45

gcg gtt tta atc tgc cac gcg ctg tcg ggc aac cat cac gtt gcg ggc 192
 Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
 50 55 60

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agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gtc 240
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
   65          70          75          80

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ggt ccc gga aaa ccg att gat acg gaa cgt ttt ttc gtg gtc ggg ttg 288
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95

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aac aat ctg ggc ggc tgc gac ggc agc agc ggg cct ttg tcg atc aat 336
Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
          100          105          110

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cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg atg gtt acg gtg 384
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Met Val Thr Val
 115 120 125

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aag gac tgg gta aaa tca caa gcc gcg ctt gcc gat tat ctc ggc atc 432
Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Ala Asp Tyr Leu Gly Ile
    130           135           140

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Glu Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala	
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Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Asp
180 185 190

gta gca cgt cag gcg att ttg acc gac ccc gat ttc aat gaa gga cat 624
 Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His
 195 200 205

tac cgc agc cac aac acc gtt ccc gcg cgc ggt ttg cg ^g att gcc cgt Tyr Arg Ser His Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg 210 215 220	672
atg atg gga cac att acg tat ctt gcc gaa gac ggt ttg ggc aaa aaa Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys 225 230 235 240	720
ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat agc gtt Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Ser Val 245 250 255	768
gaa ttt gaa gta gaa tcc tat ctc cgc tat caa ggc gac aaa ttc gtc Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val 260 265 270	816
ggg cgg ttt gat gct aat aca tat ttg ctg atg acc aaa gct ttg gac Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp 275 280 285	864
tat ttc gat ccg gcg gcg gat ttc ggc aac agc ctg acc cgc gcc gtg Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val 290 295 300	912
cag gat gtg cag gca aaa ttc ttt gtc gcc agc ttc agc acc gac tgg Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp 305 310 315 320	960
cgt ttc gcg ccc gaa cgt tcg cac gaa ctg gtc aag gca ctg att gcc Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala 325 330 335	1008
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Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn 35 40 45
Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly 50 55 60
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val 65 70 75 80

Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Met Val Thr Val
 115 120 125
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Ala Asp Tyr Leu Gly Ile
 130 135 140
 Glu Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145 150 155 160
 Leu Gln Trp Ala Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165 170 175
 Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Asp
 180 185 190
 Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His
 195 200 205
 Tyr Arg Ser His Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg
 210 215 220
 Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys
 225 230 235 240
 Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Ser Val
 245 250 255
 Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val
 260 265 270
 Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp
 275 280 285
 Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val
 290 295 300
 Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp
 305 310 315 320
 Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala
 325 330 335
 Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His
 340 345 350
 Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Thr Ala
 355 360 365
 Tyr Met Asn Asn Val Asp Lys Asp Cys Arg Leu
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 <212> DNA
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<223> RNM00815

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Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe
20 25 30

gat ctg atg att gaa acc tac ggc gag ctg aat gcc gaa aaa aat aat 144
Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
35 40 45

gcg gtt tta atc tgt cat gcg ctg tca ggc aac cat cat gtt gcg ggc 192
Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
50 55 60

agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gta 240
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
65 70 75 80

gga ccc ggc aaa ccg att gat aca gaa cgt ttt ttc gtg gtc ggt ttg 288
Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
85 90 95

aac aat ctg ggc tgc gac ggc agc agc gga cct ttg tcg atc aat 336
Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
100 105 110

cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg gtg gtt acg gtg 384
Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val
115 120 125

aag gac tgg gta aaa tcc caa gcc gcg ctt acc gat tat ctc ggc atc 432
Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile
130 135 140

ggg caa tgg gcg gcg gtt gtc ggc ggc agc ttg ggc ggt atg cag gct 480
Gly Gln Trp Ala Ala Val Val Gly Ser Leu Gly Gly Met Gln Ala
145 150 155 160

ttg cag tgg acg att tcc tat ccc gag cgc gtg cgc cat gcc tta gtg 528
Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
165 170 175

att gcg tcc gcg ccg aaa ctg tcc acg caa aat atc gcg ttt aat gat 576
Ile Ala Ser Ala Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp
180 185 190

gta gca cgt cag gcg att ttg acc gat ccc gat ttc aac gaa gga cat 624
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His
195 200 205

tac cgc agc cgc aac acc gtt ccc gct cgg ggc ttg cgg att gcc cgc 672
Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg
210 215 220

atg atg ggg cac atc acc tat ctt gcc gaa gac ggt ttg ggc aaa aaa 720
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys
225 230 235 240

ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat ggc gtt 768
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val
245 250 255

gaa ttt gaa gta gaa tcc tat ctg cgc tat caa ggc gat aaa ttc gtc Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val 260 265 270	816
ggg cgg ttt gat gcc aac acc tat ttg ctg atg acc aag gct ttg gac Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp 275 280 285	864
tat ttc gat ccg gcg gcg gat ttc ggc aac agc ctg acc cgc gcc gtg Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val 290 295 300	912
cag gat gtt cag gca aaa ttc ttt gtc gcc agc ttc agc acc gat tgg Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp 305 310 315 320	960
cgt ttc gcg ccc gaa cgt tcg cac gaa ctg gtc aag gcc ctg att gcc Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala 325 330 335	1008
gcc caa aaa tcc gtg cag tat atc gaa gtc aaa tcc gca cac ggg cac Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His 340 345 350	1056
gat gcc ttt tta atg gaa gac gaa gcc tat atg cgt gcg gtc gcc gcc Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala 355 360 365	1104
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<213> Neisseria meningitidis ser. A

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Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly 50 55 60
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val 65 70 75 80
Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu 85 90 95
Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn 100 105 110
Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val 115 120 125
Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile 130 135 140
Gly Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala

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165	170	175	
Ile Ala Ser Ala Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp			
180	185	190	
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His			
195	200	205	
Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg			
210	215	220	
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys			
225	230	235	240
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val			
245	250	255	
Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val			
260	265	270	
Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp			
275	280	285	
Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val			
290	295	300	
Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp			
305	310	315	320
Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala			
325	330	335	
Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His			
340	345	350	
Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala			
355	360	365	
Tyr Met Asn Asn Val Tyr Lys Glu Cys Gln Gln			
370	375		

<210> 15
<211> 1140
<212> DNA
<213> Pseudomonas fluorescens

<220>
<221> CDS
<222> (1)..(1137)
<223> RPU01633

<400> 15		
atg cca gct gcc ttt ccc ccc gat tct gtt ggt ctg gtg acg ccg caa		48
Met Pro Ala Ala Phe Pro Pro Asp Ser Val Gly Leu Val Thr Pro Gln		
1	5.	10
		15
acg gcg cac ttc agc gaa ccg ctg gcc ctg ggc cgt tcg ctg		
Thr Ala His Phe Ser Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu		96
20	25	30
gcc gat tat gac ctg atc tac gaa acc tac ggc acg ctg aac gcg caa		
Ala Asp Tyr Asp Leu Ile Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Gln		144
35	40	45

gct gac aac gcc gtg atc tgc cac gcc ttg tcc ggc cac cac cat Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His 50 55 60	192
gct gcg ggt tat cac agc gtc gac gac cgc aag ccc ggt tgg tgg gac Ala Ala Gly Tyr His Ser Val Asp Asp Arg Lys Pro Gly Trp Trp Asp 65 70 75 80	240
agc tgc atc ggc ccc ggc aaa ccg atc gac acc aac aag ttc ttc gtg Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Lys Phe Phe Val 85 90 95	288
gtc agc ctg aac aac ctc ggc ggt tgc aat ggt tct acc ggc ccg agc Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser 100 105 110	336
agc ctc aat ccg gaa acc ggc aag ccg ttc ggc gcc gac ttc ccg gtg Ser Leu Asn Pro Glu Thr Gly Lys Pro Phe Gly Ala Asp Phe Pro Val 115 120 125	384
ctg acc gtg gaa gac tgg gtg cac agc cag gca cgc ctg gcc gac ctg Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Leu 130 135 140	432
ctc ggc atc ggc cag tgg gcg gcg gtg atc ggc ggc agc ctg ggc ggc Leu Gly Ile Gly Gln Trp Ala Ala Val Ile Gly Gly Ser Leu Gly Gly 145 150 155 160	480
atg cag gcg ctg caa tgg acc atc acc tat ccg gat cgc gtt cgc cac Met Gln Ala Leu Gln Trp Thr Ile Thr Tyr Pro Asp Arg Val Arg His 165 170 175	528
tgc ctg gcc atc gcc tcg gcc ccc aag ctg tcg gcg cag aac atc gcc Cys Leu Ala Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala 180 185 190	576
ttc aac gaa gtg gcg cgc cag gcg atc ctc act gac ccg gaa ttc cac Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Phe His 195 200 205	624
ggc ggc tcg ttc cag gaa cac ggc gtg atc ccc aag cgc ggc ctg atg Gly Gly Ser Phe Gln Glu His Gly Val Ile Pro Lys Arg Gly Leu Met 210 215 220	672
ctg gcg cgg atg gtg ggg cac atc acc tac ctg tcc gac gac tcc atg Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met 225 230 235 240	720
ggt gag aaa ttc ggc cgt ggc ctg aag agc gaa aag ctc aac tac gac Gly Glu Lys Phe Gly Arg Gly Leu Lys Ser Glu Lys Leu Asn Tyr Asp 245 250 255	768
ttc cac agc gtc gag ttc cag gtc gaa agc tac ctg cgc tat cag ggc Phe His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly 260 265 270	816
gaa gag ttc tcc ggg cgc ttc gat gcc aac acc tat ctg ttg atg acc Glu Glu Phe Ser Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr 275 280 285	864
aag gct ctg gac tac ttc gat ccg gcg gcg aac ttc aac gat aac ctg Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Asn Phe Asn Asp Asn Leu 290 295 300	912
gct aaa acc ttc gaa ggt gca aaa gcc aag ttc tgc gtg atg tcg ttc Ala Lys Thr Phe Glu Gly Ala Lys Ala Phe Cys Val Met Ser Phe	960

305	310	315	320
acc acc gac tgg cgc ttc tcc ccg gcc cgc tcg cga gaa ctg gtg gat			
Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp			
325	330	335	
gcg ctg atg gcg gcg aaa gac gtc agc tac ctg gaa atc gac gcg			
Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala			
340	345	350	
ccc cag ggc cac gac gcc ttc ctg att ccg atc ccg cgc tac ttg cag			
Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln			
355	360	365	
gcg ttc ggc aat tac atg aac cgc att acg ttg tga			
Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu			
370	375		

<210> 16
 <211> 379
 <212> PRT
 <213> Pseudomonas fluorescens

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		15
Thr Ala His Phe Ser Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu		
20	25	30
Ala Asp Tyr Asp Leu Ile Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Gln		
35	40	45
Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His		
50	55	60
Ala Ala Gly Tyr His Ser Val Asp Asp Arg Lys Pro Gly Trp Trp Asp		
65	70	75
		80
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Lys Phe Phe Val		
85	90	95
Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser		
100	105	110
Ser Leu Asn Pro Glu Thr Gly Lys Pro Phe Gly Ala Asp Phe Pro Val		
115	120	125
Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Leu		
130	135	140
Leu Gly Ile Gly Gln Trp Ala Ala Val Ile Gly Gly Ser Leu Gly Gly		
145	150	155
		160
Met Gln Ala Leu Gln Trp Thr Ile Thr Tyr Pro Asp Arg Val Arg His		
165	170	175
Cys Leu Ala Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala		
180	185	190
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Phe His		
195	200	205
Gly Gly Ser Phe Gln Glu His Gly Val Ile Pro Lys Arg Gly Leu Met		
210	215	220

Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 Gly Glu Lys Phe Gly Arg Gly Leu Lys Ser Glu Lys Leu Asn Tyr Asp
 245 250 255
 Phe His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly
 260 265 270
 Glu Glu Phe Ser Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr
 275 280 285
 Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Asn Phe Asn Asp Asn Leu
 290 295 300
 Ala Lys Thr Phe Glu Gly Ala Lys Ala Lys Phe Cys Val Met Ser Phe
 305 310 315 320
 Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp
 325 330 335
 Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala
 340 345 350
 Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln
 355 360 365
 Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu
 370 375

<210> 17
 <211> 1140
 <212> DNA
 <213> *Pseudomonas aeruginosa*

<220>
 <221> CDS
 <222> (1)...(1137)
 <223> RPA04460

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 Met Pro Thr Val Phe Pro Asp Asp Ser Val Gly Leu Val Ser Pro Gln
 1 5 10 15
 acg ctg cac ttc aac gaa ccg ctc gag ctg acc agc ggc aag tcc ctg 96
 Thr Leu His Phe Asn Glu Pro Leu Glu Leu Thr Ser Gly Lys Ser Leu
 20 25 30
 gcc gag tac gac ctg gtg atc gaa acc tac ggc gag ctg aat gcc acg 144
 Ala Glu Tyr Asp Leu Val Ile Glu Thr Tyr Gly Glu Leu Asn Ala Thr
 35 40 45
 cag agc aac gcg gtg ctg atc tgc cac gcc ctc tcc ggc cac cac cac 192
 Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60
 gcc gcc ggc tac cac agc gtc gac gag cgc aag ccg ggc tgg tgg gac 240
 Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80
 agc tgc atc ggt ccg ggc aag ccg atc gac acc cgc aag ttc ttc gtc 288
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val
 85 90 95
 gtc gcc ctc aac aac ctc ggc ggt tgc aac gga tcc agc ggc ccc gcc 336

Val Ala Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Ser Gly Pro Ala			
100	105	110	
agc atc aat ccg gcg acc ggc aag gtc tac ggc gcg gac ttc ccg atg		384	
Ser Ile Asn Pro Ala Thr Gly Lys Val Tyr Gly Ala Asp Phe Pro Met			
115	120	125	
gtt acg gtg gaa gac tgg gtg cat agc cag gcg cgc ctg gca gac cgc		432	
Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg			
130	135	140	
ctc ggc atc cgc cag tgg gcc gcg gtg gtc ggc ggc agc ctc ggc ggc		480	
Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly			
145	150	155	160
atg cag gcg ctg caa tgg acc atc agc tat ccc gag cgc gtc cgt cac		528	
Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His			
165	170	175	
tgc ctg tgc atc gcc agc gcg ccg aag ctg tcg gcg cag aac atc gcc		576	
Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala			
180	185	190	
ttc aac gaa gtc gcc cg ^g cag gcg att ctt tcc gac cct gag ttc ctc		624	
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu			
195	200	205	
ggc ggc tac ttc cag gag cag ggc gtg att ccc aag cgc ggc ctc aag		672	
Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys			
210	215	220	
ctg gcg cg ^g atg gtc ggc cat atc acc tac ctg tcc gac gac gcc atg		720	
Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met			
225	230	235	240
ggc gcc aag ttc ggc cgt gta ctg aag acc gag aag ctc aac tac gac		768	
Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp			
245	250	255	
ctg cac agc gtc gag ttc cag gtc gag agt tac ctg cgc tac cag ggc		816	
Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly			
260	265	270	
gag gag ttc tcc acc cgc ttc gac gcc aat acc tac ctg ctg atg acc		864	
Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr			
275	280	285	
aag gcg ctg gac tac ttc gac ccc gcc gcc cac ggc gac gac ctg		912	
Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala His Gly Asp Asp Leu			
290	295	300	
gtg cgc acc ctg gag ggc gtc gag gcg gac ttc tgc ctg atg tcc ttc		960	
Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe			
305	310	315	320
acc acc gac tgg cgt ttc tcg ccg gcc cgc tcg cgg gaa atc gtc gac		1008	
Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp			
325	330	335	
gcc ctg atc gcg gcg aaa aag aac gtc agc tac ctg gag atc gac gcc		1056	
Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala			
340	345	350	
ccg caa ggc cac gac gcc ttc ctc atg ccg atc ccc cgg tac ctg caa		1104	
Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln			
355	360	365	

gcc ttc agc ggt tac atg aac cgc atc agc gtg tga 1140
 Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
 370 375

 <210> 18
 <211> 379
 <212> PRT
 <213> Pseudomonas aeruginosa

 <400> 18
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 Thr Leu His Phe Asn Glu Pro Leu Glu Leu Thr Ser Gly Lys Ser Leu 20 25 30
 Ala Glu Tyr Asp Leu Val Ile Glu Thr Tyr Gly Glu Leu Asn Ala Thr 35 40 45
 Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His 50 55 60
 Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp 65 70 75 80
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val 85 90 95
 Val Ala Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Ser Gly Pro Ala 100 105 110
 Ser Ile Asn Pro Ala Thr Gly Lys Val Tyr Gly Ala Asp Phe Pro Met 115 120 125
 Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg 130 135 140
 Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His 165 170 175
 Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu 195 200 205
 Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys 210 215 220
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met 225 230 235 240
 Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp 245 250 255
 Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly 260 265 270
 Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr 275 280 285
 Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Ala His Gly Asp Asp Leu 290 295 300

Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe
 305 310 315 320

Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp
 325 330 335

Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala
 340 345 350

Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln
 355 360 365

Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
 370 375

<210> 19

<211> 1146

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (1)...(1143)

<223> RBU12675

<400> 19

atg gaa tcg atc ggt atc gtc gct ccc caa aaa atg cat ttc acc gag	48
Met Glu Ser Ile Gly Ile Val Ala Pro Gln Lys Met His Phe Thr Glu	
1 5 10 15	

ccg ctg ccg ttg cag aac ggc agt tcg ctc gcc ggt tac gac ctg atg	96
Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met	
20 25 30	

gtc gag acc tac ggc acg ctc aac gcc gcg cgt agc aac gcg gtg ctg	144
Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu	
35 40 45	

gtg tgc cac gcg ctc aac gcg tcg cac cac gtg gcg ggc gtg tat gcc	192
Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala	
50 55 60	

gac aac ccc agg gac atc ggc tgg tgg gac aac atg gtc ggc ccg ggc	240
Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly	
65 70 75 80	

aag ccg ctc gac act gac aag ttc ttc gtg atc ggc gtg aac aac ctc	288
Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu	
85 90 95	

gga tcg tgc ttc ggc tcg act ggg ccg atg agc atc gat ccg tct acc	336
Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr	
100 105 110	

ggc aat ccg tac ggc gcg acg ttt ccc gtc gtg acg gtg gaa gac tgg	384
Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp	
115 120 125	

gtc aac gcc cag gcg cgc gtc gcg gat caa ttc ggc atc acg cgc ttt	432
Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe	
130 135 140	

gcg gcg gtg atg ggc ggc agc ctc ggc ggc atg cag gcg ctc gcg tgg	480
Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp	
145 150 155 160	

agc atg atg tat ccg gag cgc gtc gct cac tgc atc gtg gtc gcg tcc Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser	165 170 175	528
aca ccc aag ctg tcg gcg cag aac atc gcg ttc aac gag gtt gcg cgc Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg	180 185 190	576
tcg gcg atc ctg tcg gac ccg gac ttc cac ggc ggc aac tac tac gcg Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala	195 200 205	624
cac aac gtt aag ccg aag cgc ggc ctg cgc gtc gcg cgc atg atc ggc His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly	210 215 220	672
cac atc acg tat ctg tcg gac gac atg gcc gag aaa ttc ggc cgc His Ile Thr Tyr Leu Ser Asp Asp Asp Met Ala Glu Lys Phe Gly Arg	225 230 235 240	720
tcg ctg cgg cgc gcg gaa ggc gcg ctg gac gcg tac aac ttc aac ttc Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe	245 250 255	768
gac gtg gag ttc gag gtg gag tcg tac ctg cgc tac cag ggc gac aag Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys	260 265 270	816
ttc gcc gac tac ttc gac gcg aat acg tat ctg ctg atc acc cgc gcg Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala	275 280 285	864
ctc gac tac ttc gat ccg gcc aag gcc ttc gcc ggc gac ctg acg gcc Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala	290 295 300	912
gcg gtc gcg cac acc acg gcg aaa tat ctg atc gcc agc ttc acg acc Ala Val Ala His Thr Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr	305 310 315 320	960
gac tgg cgc ttc gcg ccg gcc cgc tcg cgt gaa ctg gtg aag gcg ctg Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu	325 330 335	1008
ctc gat cac aag cgc acg gtc acc tac gcg gaa atc gac gcg ccg cac Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His	340 345 350	1056
ggc cac gac gcc ttc ctg ctc gac gac gcg cgc tat cac aac ctg atg Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met	355 360 365	1104
cgc gct tac tac gaa cgt att gcg aac gag gtg aac gca tga Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala	370 375 380	1146

<210> 20
<211> 381
<212> PRT
<213> Burkholderia cepacia

<400> 20
Met Glu Ser Ile Gly Ile Val Ala Pro Gln Lys Met His Phe Thr Glu
1 5 10 15

Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met
 20 25 30

Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu
 35 40 45

Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala
 50 55 60

Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly
 65 70 75 80

Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu
 85 90 95

Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr
 100 105 110

Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp
 115 120 125

Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe
 130 135 140

Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp
 145 150 155 160

Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser
 165 170 175

Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg
 180 185 190

Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala
 195 200 205

His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly
 210 215 220

His Ile Thr Tyr Leu Ser Asp Asp Asp Met Ala Glu Lys Phe Gly Arg
 225 230 235 240

Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe
 245 250 255

Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys
 260 265 270

Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala
 275 280 285

Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala
 290 295 300

Ala Val Ala His Thr Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr
 305 310 315 320

Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu
 325 330 335

Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His
 340 345 350

Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met
 355 360 365

Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala

370

375

380

<210> 21
<211> 1134
<212> DNA
<213> *Nitrosomonas europaea*

<220>
<221> CDS
<222> (1)..(1131)
<223> RNE02005

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Met Ser Thr Gln Asp Ser Asp Ser Ile Gly Ile Val Ser Ala Arg Arg
   1           5           10          15

```

gcc cat ttc gac acc ccg ctc agc ctg aaa agc gga gct gta ctg gac 96
Ala His Phe Asp Thr Pro Leu Ser Leu Lys Ser Gly Ala Val Leu Asp
20 25 30

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agc tac gag ctc gtc tat gaa acc tat ggg gag ctg aat gca gac cga 144
Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Glu Leu Asn Ala Asp Arg
          35           40           45

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tcc aat gca gtg ctg atc tgc cat gct tta tcc ggc aac cac cat gtt	192
Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val	
50 55 60	

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gcc ggt gtt tat gca gat aac ccc aag aat acc gga tgg tgg aac aac 240
Ala Gly Val Tyr Ala Asp Asn Pro Lys Asn Thr Gly Trp Trp Asn Asn
   65           70           75           80

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atg atc ggt ccg ggc aaa ccg gtc gat acc cga aaa ttc ttt gtc atc 288
Met Ile Gly Pro Gly Lys Pro Val Asp Thr Arg Lys Phe Phe Val Ile
85          90          95

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ggt atc aat aat ctc ggg ggt tgc cat ggc tcc acc ggg ccc atc agc 336
Gly Ile Asn Asn Leu Gly Gly Cys His Gly Ser Thr Gly Pro Ile Ser
          100           105           110

```

atc aac gac aag acc ggt aaa cgc ttc ggc ccg gat ttt ccg ctg gta 384
Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val
115 120 125

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acg aca gct gac tgg gca aaa acc tat gtc cgt ttc gcc gat cag ttc 432
Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe
      130          135          140

```

```

agc atc gac tgt ttt gcc gcc gtc atc ggt ggc agt ctg ggc ggg atg 480
Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Gly Ser Leu Gly Gly Met
145           150           155           160

```

```

tcg gcc atg caa ctg gcg ctc gat gca ccg gaa aga gtt cgt cat gcc 528
Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala
165          170          175

```

```

ata gtg gtt gca gca tcg gcc agg ctg aca gca cag aac atc gct ttc 576
Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe
180          185          190

```

```

aat gat gtc gcg cgt cag gcg att ctg acc gac cct gat ttt cac gac 624
Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp
          195           200           205

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ggc gac tat tat tcc cat ggc acc cac ccg cgc aga ggt tta cgc ctt 672

Gly Asp Tyr Tyr Ser His Gly Thr His Pro Arg Arg Gly Leu Arg Leu						
210	215	220				
gcc cgc atg ctt ggc cac atc acc tac ctg tcg gac gac tcc atg gcc						720
Ala Arg Met Leu Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met Ala						
225	230	235	240			
agc aaa ttc ggc cgt gag tta cgt aac ggc tcg ctt gct ttc aat tat						768
Ser Lys Phe Gly Arg Glu Leu Arg Asn Gly Ser Leu Ala Phe Asn Tyr						
245	250	255				
gat gtg gaa ttc cag atc gaa tcc tat ctg cac cat cag ggc gac aaa						816
Asp Val Glu Phe Gln Ile Glu Ser Tyr Leu His His Gln Gly Asp Lys						
260	265	270				
ttt gcc gac ctg ttc gac gca aac act tat ctg ctg atg acg aag gcg						864
Phe Ala Asp Leu Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala						
275	280	285				
ctc gat tat ttc gat ccg gcc cag gat tac gat ggc aac ctg agt gca						912
Leu Asp Tyr Phe Asp Pro Ala Gln Asp Tyr Asp Gly Asn Leu Ser Ala						
290	295	300				
gcc ttt gcc cgt gca caa gcg gat ttt ctg gta ctt tcc ttt act tcc						960
Ala Phe Ala Arg Ala Gln Ala Asp Phe Leu Val Leu Ser Phe Thr Ser						
305	310	315	320			
gac tgg cgt ttt tcc ccg gag cgt tcg cgc gat atc gtc aag gca ctg						1008
Asp Trp Arg Phe Ser Pro Glu Arg Ser Arg Asp Ile Val Lys Ala Leu						
325	330	335				
ctc gac aac aaa ctg aat gtc agt tat gcg gaa att ccc tcc tcg tac						1056
Leu Asp Asn Lys Leu Asn Val Ser Tyr Ala Glu Ile Pro Ser Ser Tyr						
340	345	350				
gga cat gat tcc ttt ctc atg cag gac gac tac tat cac cag ttg ata						1104
Gly His Asp Ser Phe Leu Met Gln Asp Asp Tyr Tyr His Gln Leu Ile						
355	360	365				
cgt gct tac atg aac aat atc gct ctc tag						1134
Arg Ala Tyr Met Asn Asn Ile Ala Leu						
370	375					

<210> 22
<211> 377
<212> PRT
<213> Nitrosomonas europaea

<400> 22						
Met Ser Thr Gln Asp Ser Asp Ser Ile Gly Ile Val Ser Ala Arg Arg						
1	5	10	15			
Ala His Phe Asp Thr Pro Leu Ser Leu Lys Ser Gly Ala Val Leu Asp						
20	25	30				
Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Glu Leu Asn Ala Asp Arg						
35	40	45				
Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val						
50	55	60				
Ala Gly Val Tyr Ala Asp Asn Pro Lys Asn Thr Gly Trp Trp Asn Asn						
65	70	75	80			
Met Ile Gly Pro Gly Lys Pro Val Asp Thr Arg Lys Phe Phe Val Ile						
85	90	95				

Gly Ile Asn Asn Leu Gly Gly Cys His Gly Ser Thr Gly Pro Ile Ser
 100 105 110
 Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val
 115 120 125
 Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe
 130 135 140
 Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Gly Ser Leu Gly Gly Met
 145 150 155 160
 Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala
 165 170 175
 Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe
 180 185 190
 Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp
 195 200 205
 Gly Asp Tyr Tyr Ser His Gly Thr His Pro Arg Arg Gly Leu Arg Leu
 210 215 220
 Ala Arg Met Leu Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met Ala
 225 230 235 240
 Ser Lys Phe Gly Arg Glu Leu Arg Asn Gly Ser Leu Ala Phe Asn Tyr
 245 250 255
 Asp Val Glu Phe Gln Ile Glu Ser Tyr Leu His His Gln Gly Asp Lys
 260 265 270
 Phe Ala Asp Leu Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala
 275 280 285
 Leu Asp Tyr Phe Asp Pro Ala Gln Asp Tyr Asp Gly Asn Leu Ser Ala
 290 295 300
 Ala Phe Ala Arg Ala Gln Ala Asp Phe Leu Val Leu Ser Phe Thr Ser
 305 310 315 320
 Asp Trp Arg Phe Ser Pro Glu Arg Ser Arg Asp Ile Val Lys Ala Leu
 325 330 335
 Leu Asp Asn Lys Leu Asn Val Ser Tyr Ala Glu Ile Pro Ser Ser Tyr
 340 345 350
 Gly His Asp Ser Phe Leu Met Gln Asp Asp Tyr Tyr His Gln Leu Ile
 355 360 365
 Arg Ala Tyr Met Asn Asn Ile Ala Leu
 370 375

<210> 23
 <211> 1077
 <212> DNA
 <213> Haemophilus influenzae

<220>
 <221> CDS
 <222> (1)...(1074)
 <223> RHI02681
 <400> 23

atg tct gtg caa aat gta gtg ctt ttt gac aca cag cct tta act ctg Met Ser Val Gln Asn Val Val Leu Phe Asp Thr Gln Pro Leu Thr Leu 1 5 10 15	48
atg ctt ggc ggc aaa ctt tcc cat att aat gtc gcg tat caa act tat Met Leu Gly Gly Lys Leu Ser His Ile Asn Val Ala Tyr Gln Thr Tyr 20 25 30	96
ggc acg ctc aat gcc gaa aaa aat aat gcg gta tta att tgc cac gct Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala 35 40 45	144
ttg act ggt gat gct gag cct tat ttc gat gat ggt cga gat ggc tgg Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp 50 55 60	192
tgg cag aat ttt atg gga gca ggt tta gca ttg gat acg gat cgt tat Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr 65 70 75 80	240
ttt ttt att agc tcg aac gta tta ggt ggt tgc aag gga aca act ggg Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly 85 90 95	288
cct tca tca att aat ccg caa acg ggt aaa cct tat ggc agc caa ttt Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe 100 105 110	336
cct aat att gtt gtg caa gat att gtt aaa gta caa aaa gcc ttg ctt Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu 115 120 125	384
gat cat ctt ggt att agc cat tta aaa gcc att att ggt gga tct ttt Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe 130 135 140	432
ggc ggc atg caa gcg aat caa tgg gcg att gat tat cct gat ttt atg Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met 145 150 155 160	480
gat aat atc gtg aat ctt tgc tca tcc att tat ttt agt gct gaa gcc Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala 165 170 175	528
ata ggt ttt aat cac gta atg cgt caa gcg gtc att aat gat ccc aat Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn 180 185 190	576
ttt aac ggc ggc gat tat tat gag ggt aca ccg cca gat caa ggg tta Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu 195 200 205	624
tct att gca cgt atg cta ggt atg ctg act tac cgc acc gat tta caa Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln 210 215 220	672
ctt gcg aaa gcc ttt ggg cgt gcc aca aaa tca gat ggc agc ttt tgg Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp 225 230 235 240	720
ggc gat tac ttt caa gtg gaa tcc tat ctt tct tac caa ggc aaa aaa Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys 245 250 255	768
ttc tta gaa cgt ttt gat gcc aat agt tat ttg cat ttg tta cgt gcg Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Leu Arg Ala 260 265 270	816

ttg gat atg tat gat cca agt ttg ggg tat gac aat gtt aaa gag gca Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala 275	280	285	864
tta tca cgt att aaa gca cgc tat acg ttg gtt tct gtg aca acg gat Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp 290	295	300	912
caa ctt ttt aaa ccc att gat ctt tat aaa agt aaa cag ctt tta gag Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu 305	310	315	960
caa agt gga gtc gat cta cat ttt tat gaa ttc cca tca gat tac gga Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly 325	330	335	1008
cac gat gcg ttt tta gtg gat tat gat cag ttt gaa aaa cga att cga His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg 340	345	350	1056
gat ggt ttg gca ggt aat taa Asp Gly Leu Ala Gly Asn 355			1077

<210> 24
<211> 358
<212> PRT
<213> Haemophilus influenzae

<400> 24 Met Ser Val Gln Asn Val Val Leu Phe Asp Thr Gln Pro Leu Thr Leu 1 5 10 15			
Met Leu Gly Gly Lys Leu Ser His Ile Asn Val Ala Tyr Gln Thr Tyr 20 25 30			
Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala 35 40 45			
Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp 50 55 60			
Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr 65 70 75 80			
Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly 85 90 95			
Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe 100 105 110			
Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu 115 120 125			
Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe 130 135 140			
Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met 145 150 155 160			
Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala 165 170 175			
Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn 180 185 190			

Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu
 195 200 205

Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln
 210 215 220

Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp
 225 230 235 240

Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys
 245 250 255

Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Leu Arg Ala
 260 265 270

Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala
 275 280 285

Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp
 290 295 300

Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu
 305 310 315 320

Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly
 325 330 335

His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg
 340 345 350

Asp Gly Leu Ala Gly Asn
 355

<210> 25

<211> 1296

<212> DNA

<213> Halobacterium sp

<220>

<221> CDS

<222> (1)..(1293)

<223> ETX_HALN1

<400> 25

atg ggc cac gat cac gga ctc cac acc aac agt gta cac gcc ggc cag	48
Met Gly His Asp His Gly Leu His Thr Asn Ser Val His Ala Gly Gln	
1 5 10 15	

cgc gtc gac ccg gcc acg ggc gct cgc gcg ccg cca ctc tac cag acc	96
Arg Val Asp Pro Ala Thr Gly Ala Arg Ala Pro Pro Leu Tyr Gln Thr	
20 25 30	

acg tcg tac gcc ttc gag gac agc gcc gat gcc gcc ggc cag ttc gcc	144
Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala	
35 40 45	

ctt gag cgg gac ggc tac atc tac tcg cgg ctg atg aac ccc acc gtg	192
Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val	
50 55 60	

gag acc ctc cag gac cgc ctc gcc gcc ctc gaa ggc ggc gtc ggc gcg	240
Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala	
65 70 75 80	

gtc gcc acc gcg tcc gga atg gcc gcc ctg gac ctc gcg acg ttc ctg 288

Val Ala Thr Ala Ser Gly Met Ala Ala Leu Asp Leu Ala Thr Phe Leu			
85	90	95	
ctg gca cgc gcc ggc gac tcc gtc gtc gcc gcc agc gac ctc tac ggc			336
Leu Ala Arg Ala Gly Asp Ser Val Val Ala Ala Ser Asp Leu Tyr Gly			
100	105	110	
ggc acc gtg acg tac ctc acg cac agc gcc cag cgc cgc ggc gtc gac			384
Gly Thr Val Thr Tyr Leu Thr His Ser Ala Gln Arg Arg Gly Val Asp			
115	120	125	
acg acg ttc gtg gac gtc ctc gac tac gac gcc tac gcc gac gcc atc			432
Thr Thr Phe Val Asp Val Leu Asp Tyr Asp Ala Tyr Ala Asp Ala Ile			
130	135	140	
gac gcc gac acc gcc tac gtg ctc gtc gaa acc gtc ggc aac ccc agc			480
Asp Ala Asp Thr Ala Tyr Val Leu Val Glu Thr Val Gly Asn Pro Ser			
145	150	155	160
ctg atc acg ccc gac ctc gaa cgc atc gcc gac atc gcc cac gac aac			528
Leu Ile Thr Pro Asp Leu Glu Arg Ile Ala Asp Ile Ala His Asp Asn			
165	170	175	
ggc gtt ccc ctg ctg gtg gac aac acg ttc gcg acc ccc gcg ctg gca			576
Gly Val Pro Leu Leu Val Asp Asn Thr Phe Ala Thr Pro Ala Leu Ala			
180	185	190	
acc ccg atc gac cac ggt gcc gac atc gtc tgg cac tcc acc acc aaa			624
Thr Pro Ile Asp His Gly Ala Asp Ile Val Trp His Ser Thr Thr Lys			
195	200	205	
tgg atc cac ggt gcc ggc acc acc gtc ggc ggc ctc gtc gac gcc			672
Trp Ile His Gly Ala Gly Thr Thr Val Gly Gly Ala Leu Val Asp Ala			
210	215	220	
ggc agc ttc gac tgg gac gcc cac gcc gac tac ccc gag atc gcc			720
Gly Ser Phe Asp Trp Asp Ala His Ala Asp Tyr Pro Glu Ile Ala			
225	230	235	240
cag gaa aac ccc gcc tac cac ggc gtg acc ttc acc gat cgc ttc ggg			768
Gln Glu Asn Pro Ala Tyr His Gly Val Thr Phe Thr Asp Arg Phe Gly			
245	250	255	
gac gcc gcg ttc acg tac gcc gca atc gcc cgc ggg ctg cgc gat ctg			816
Asp Ala Ala Phe Thr Tyr Ala Ala Ile Ala Arg Gly Leu Arg Asp Leu			
260	265	270	
ggc aac cag cag tcg ccg ttc gac gcc tgg cag acc ctc cag aag ctc			864
Gly Asn Gln Gln Ser Pro Phe Asp Ala Trp Gln Thr Leu Gln Lys Leu			
275	280	285	
gaa acg ctc ccg ctg cgc atg caa caa cac tgc cgg aac gcc cag ctc			912
Glu Thr Leu Pro Leu Arg Met Gln Gln His Cys Arg Asn Ala Gln Leu			
290	295	300	
gtc gcc gaa cac ctc cgg gac cac ccc aac gtg tcg tgg gtc aac tac			960
Val Ala Glu His Leu Arg Asp His Pro Asn Val Ser Trp Val Asn Tyr			
305	310	315	320
ccc ggg ctg gcc gac cac gac acc cac gac aac gca acc acc tac ctc			1008
Pro Gly Leu Ala Asp His Asp Thr His Asp Asn Ala Thr Thr Tyr Leu			
325	330	335	
gat tcg ggc tac gga ggc atg ctc acg ttc ggc gtc gag gac ggc tac			1056
Asp Ser Gly Tyr Gly Gly Met Leu Thr Phe Gly Val Glu Asp Gly Tyr			
340	345	350	

gag gcc gcc caa tcg gtc acc gag gag acc acg ctt gcc agc ctg ctg	1104
Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu	
355 360 365	
gcg aac gtc ggc gac gcc aaa acg ctc gtg atc cac ccc gcc tcc acc	1152
Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr	
370 375 380	
acc cac cag cag ctc acc ccc gaa gcc cag cgc gcc ggc ggt gtg cgc	1200
Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg	
385 390 395 400	
ccc gag atg gtg cgg gtg tcg gtc ggc atc gag gac ccc gcc gac atc	1248
Pro Glu Met Val Arg Val Ser Val Gly Ile Glu Asp Pro Ala Asp Ile	
405 410 415	
gtc gcg gac ctc gaa acc gcc atc gag gcc gcg gtc ggg tcg gcg	1293
Val Ala Asp Leu Glu Thr Ala Ile Glu Ala Ala Val Gly Ser Ala	
420 425 430	
tag	1296

<210> 26
<211> 431
<212> PRT
<213> Halobacterium sp

<400> 26	
Met Gly His Asp His Gly Leu His Thr Asn Ser Val His Ala Gly Gln	
1 5 10 15	
Arg Val Asp Pro Ala Thr Gly Ala Arg Ala Pro Pro Leu Tyr Gln Thr	
20 25 30	
Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala	
35 40 45	
Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val	
50 55 60	
Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala	
65 70 75 80	
Val Ala Thr Ala Ser Gly Met Ala Ala Leu Asp Leu Ala Thr Phe Leu	
85 90 95	
Leu Ala Arg Ala Gly Asp Ser Val Val Ala Ala Ser Asp Leu Tyr Gly	
100 105 110	
Gly Thr Val Thr Tyr Leu Thr His Ser Ala Gln Arg Arg Gly Val Asp	
115 120 125	
Thr Thr Phe Val Asp Val Leu Asp Tyr Asp Ala Tyr Ala Asp Ala Ile	
130 135 140	
Asp Ala Asp Thr Ala Tyr Val Leu Val Glu Thr Val Gly Asn Pro Ser	
145 150 155 160	
Leu Ile Thr Pro Asp Leu Glu Arg Ile Ala Asp Ile Ala His Asp Asn	
165 170 175	
Gly Val Pro Leu Leu Val Asp Asn Thr Phe Ala Thr Pro Ala Leu Ala	
180 185 190	
Thr Pro Ile Asp His Gly Ala Asp Ile Val Trp His Ser Thr Thr Lys	
195 200 205	

Trp Ile His Gly Ala Gly Thr Thr Val Gly Gly Ala Leu Val Asp Ala
 210 215 220

Gly Ser Phe Asp Trp Asp Ala His Ala Ala Asp Tyr Pro Glu Ile Ala
 225 230 235 240

Gln Glu Asn Pro Ala Tyr His Gly Val Thr Phe Thr Asp Arg Phe Gly
 245 250 255

Asp Ala Ala Phe Thr Tyr Ala Ala Ile Ala Arg Gly Leu Arg Asp Leu
 260 265 270

Gly Asn Gln Gln Ser Pro Phe Asp Ala Trp Gln Thr Leu Gln Lys Leu
 275 280 285

Glu Thr Leu Pro Leu Arg Met Gln Gln His Cys Arg Asn Ala Gln Leu
 290 295 300

Val Ala Glu His Leu Arg Asp His Pro Asn Val Ser Trp Val Asn Tyr
 305 310 315 320

Pro Gly Leu Ala Asp His Asp Thr His Asp Asn Ala Thr Thr Tyr Leu
 325 330 335

Asp Ser Gly Tyr Gly Gly Met Leu Thr Phe Gly Val Glu Asp Gly Tyr
 340 345 350

Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu
 355 360 365

Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr
 370 375 380

Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg
 385 390 395 400

Pro Glu Met Val Arg Val Ser Val Gly Ile Glu Asp Pro Ala Asp Ile
 405 410 415

Val Ala Asp Leu Glu Thr Ala Ile Glu Ala Ala Val Gly Ser Ala
 420 425 430

<210> 27

<211> 1143

<212> DNA

<213> Thermus thermophilus

<220>

<221> CDS

<222> (1)..(1140)

<223> RTT00268

<400> 27

atg agc gag atc gcc ctc gag gcc tgg ggg gag cac gag gcc ctc ctc 48
 Met Ser Glu Ile Ala Leu Glu Ala Trp Gly Glu His Glu Ala Leu Leu
 1 5 10 15

ctc aag ccc ccc cgc tcc ccc ctc tcc atc ccc ccc aag ccc cgc 96
 Leu Lys Pro Pro Arg Ser Pro Leu Ser Ile Pro Pro Pro Lys Pro Arg
 20 25 30

acc gcc gtc ctc ttc ccc agg cgg gag ggg ttc tac acg gag ctc ggg 144
 Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly
 35 40 45

ggg tac ctc ccc gag gtg cgc ctc cgc ttt gag acc tac ggg acc ctc Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu	50 55 60	192
tcc cgc agg cgg gat aac gcc gtc ctc gtc ttc cac gcc ctc acg ggg Ser Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly	65 70 75 80	240
agc gcc cac ctg gcg ggg acc tac gac gag gaa acc ttt aga agc ctc Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Glu Thr Phe Arg Ser Leu	85 90 95	288
tcc ccc ctg gag cag gcc ttc ggc cgg gaa ggg tgg tgg gac agc ctg Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu	100 105 110	336
gtg ggg ccc ggg cgg atc ctg gac ccc gcc ctc tac tac gtg gtc tcc Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser	115 120 125	384
gcc aac cac ctg gga agc tgc tac ggc tcc acc ggc ccc ctc tcc cta Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu	130 135 140	432
gac ccc cac acg ggc cgc ccc tac ggg agg gac ttc cct ccc ctt acc Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr	145 150 155 160	480
atc cgc gac ctg gcc cgg gcc cag gcg agg ctt ctg gac cat ctg ggg Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly	165 170 175	528
gtg gag aag gcc atc gtc atc ggg ggg agc ctc ggg ggg atg gtg gcc Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala	180 185 190	576
ctg gag ttc gcc ctc atg tac ccg gag agg gtg aag aag ctc gtg gtc Leu Glu Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val	195 200 205	624
ctg gcg gcc ccc gca cgg cac ggc ccc tgg gcc cgg gcc ttc aac cac Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His	210 215 220	672
ctc tcc cgc cag gcc atc ctc caa gac ccc gag tac cag aag ggc aac Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn	225 230 235 240	720
cct gcc ccc aag ggc atg gcc ctc gcc cgg gga atc gcc atg atg agc Pro Ala Pro Lys Gly Met Ala Leu Ala Arg Gly Ile Ala Met Met Ser	245 250 255	768
tac cgg gcc ccc gag ggg ttt gag gcc cgc tgg ggc gcg gag ccc gag Tyr Arg Ala Pro Glu Gly Phe Glu Ala Arg Trp Gly Ala Glu Pro Glu	260 265 270	816
ctc ggg gaa atc cac ctg gac tac cag ggg gag aag ttc ctc cgg cgc Leu Gly Glu Ile His Leu Asp Tyr Gln Gly Glu Lys Phe Leu Arg Arg	275 280 285	864
ttc cac gcc gag agc tac ctc gtc ctc tcc cgg gcc atg gac aac cac Phe His Ala Glu Ser Tyr Leu Val Leu Ser Arg Ala Met Asp Asn His	290 295 300	912
gac gtg ggc cgg ggc cgg ggc ggg gtg gag gag gac ctc aag cgc ctc Asp Val Gly Arg Gly Arg Gly Val Glu Glu Ala Leu Lys Arg Leu	305 310 315 320	960

agg gcc atc ccc tcc ctc ttc gtg ggc att gac acc gac ctc ctc tac Arg Ala Ile Pro Ser Leu Phe Val Gly Ile Asp Thr Asp Leu Leu Tyr 325 330 335	1008
ccc gcc tgg gag gtg agg cag gcg gcc aag gcg ggc ggg gcc cgcc tac Pro Ala Trp Glu Val Arg Gln Ala Ala Lys Ala Ala Gly Ala Arg Tyr 340 345 350	1056
cgg gag atc aaa agc ccc cac ggg cac gac gcc ttc ctc ata gag acc Arg Glu Ile Lys Ser Pro His Gly His Asp Ala Phe Leu Ile Glu Thr 355 360 365	1104
gac cag gtg gag gag atc ctg gac gcc ttc ctc ccg tag Asp Gln Val Glu Glu Ile Leu Asp Ala Phe Leu Pro 370 375 380	1143
<210> 28	
<211> 380	
<212> PRT	
<213> Thermus thermophilus	
<400> 28	
Met Ser Glu Ile Ala Leu Glu Ala Trp Gly Glu His Glu Ala Leu Leu 1 5 10 15	
Leu Lys Pro Pro Arg Ser Pro Leu Ser Ile Pro Pro Pro Lys Pro Arg 20 25 30	
Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly 35 40 45	
Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu 50 55 60	
Ser Arg Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly 65 70 75 80	
Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Glu Thr Phe Arg Ser Leu 85 90 95	
Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu 100 105 110	
Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser 115 120 125	
Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu 130 135 140	
Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr 145 150 155 160	
Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly 165 170 175	
Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala 180 185 190	
Leu Glu Phe Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val 195 200 205	
Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His 210 215 220	
Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn	

225	230	235	240
Pro Ala Pro Lys Gly Met Ala Leu Ala Arg Gly Ile Ala Met Met Ser			
245		250	255
Tyr Arg Ala Pro Glu Gly Phe Glu Ala Arg Trp Gly Ala Glu Pro Glu			
260		265	270
Leu Gly Glu Ile His Leu Asp Tyr Gln Gly Glu Lys Phe Leu Arg Arg			
275		280	285
Phe His Ala Glu Ser Tyr Leu Val Leu Ser Arg Ala Met Asp Asn His			
290		295	300
Asp Val Gly Arg Gly Arg Gly Val Glu Ala Leu Lys Arg Leu			
305	310	315	320
Arg Ala Ile Pro Ser Leu Phe Val Gly Ile Asp Thr Asp Leu Leu Tyr			
325		330	335
Pro Ala Trp Glu Val Arg Gln Ala Ala Lys Ala Ala Gly Ala Arg Tyr			
340		345	350
Arg Glu Ile Lys Ser Pro His Gly His Asp Ala Phe Leu Ile Glu Thr			
355	360	365	
Asp Gln Val Glu Glu Ile Leu Asp Ala Phe Leu Pro			
370	375	380	

<210> 29
 <211> 1005
 <212> DNA
 <213> Deinococcus radiodurans

<220>
 <221> CDS
 <222> (1)...(1002)
 <223> RDR01287

<400> 29			
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Val Thr Ala Val Leu Ala Gly His Ala Ser Ala Leu Leu Leu Thr Glu			
1	5	10	15
gaa ccc gac tgt tcg ggg ccg cag acg gtc gtt ctc ttc cggt cgt gag 96			
Glu Pro Asp Cys Ser Gly Pro Gln Thr Val Val Leu Phe Arg Arg Glu			
20	25	30	
ccg ctg ctg ctc gac tgc gga cgg gcg ctg agc gac gtg cgg gtg gcc 144			
Pro Leu Leu Asp Cys Gly Arg Ala Leu Ser Asp Val Arg Val Ala			
35	40	45	
ttt cac acc tac ggc acg ccg cgc gcc gac acg ctg gtg ctg cac 192			
Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His			
50	55	60	
gcc ctg acc ggc gac agc gcg gtg cac gag tgg tgg ccc gac ttt ctg 240			
Ala Leu Thr Gly Asp Ser Ala Val His Glu Trp Trp Pro Asp Phe Leu			
65	70	75	80
ggc gcg ggc cgg cca ctg gac ccg gca gac gac tac gtg gtg tgc gcc 288			
Gly Ala Gly Arg Pro Leu Asp Pro Ala Asp Asp Tyr Val Val Cys Ala			
85	90	95	
aac gtc ctc ggc ggg tgc gcc ggc acg acg agc gac gct gaa ctc gcc 336			
Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala			

100	105	110	
gcc acc tgt tcc gga ccg gtg ccg ctc agc ctg cgc gac atg gcc cg			384
Ala Thr Cys Ser Gly Pro Val Pro Leu Ser Leu Arg Asp Met Ala Arg			
115	120	125	
gtg ggg cgc gcc ctg ctg gat tct ctc ggc gtg cga cggtt gtc			432
Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val			
130	135	140	
atc ggc gcg agc atg ggc ggg atg ctc gcc tac gcc tgg ctg ctg gag			480
Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu			
145	150	155	160
tgc ccc gac ctg gtg gaa aag gcc gtg att ata gga gcc ccc gcg cg			528
Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg			
165	170	175	
cac tcg ccc tgg gct att gga ctg aac acg gcg gcc cgc agc gcc att			576
His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile			
180	185	190	
gcc ctc gct ccc ggc ggc gag ggg ctg aag gtg gcg cgc cag att gcc			624
Ala Leu Ala Pro Gly Gly Leu Lys Val Ala Arg Gln Ile Ala			
195	200	205	
atg ctc agt tac cgc agc ccc gaa agc cta agc cgc acg cag gcg ggg			672
Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly			
210	215	220	
cag cgc gtg ccg ggg gtg ccc gcc gtt acg tct tac ctg cac tac caa			720
Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln			
225	230	235	240
ggc gaa aaa ctc gcc gcc cgc ttc gac gag cag acc tac tgc gcc ctc			768
Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu			
245	250	255	
acc tgg gcg atg gac gcc ttt cag ccg agc agc gcc gac ctc aaa gcg			816
Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala			
260	265	270	
gtg cgc gcg ccg gta ctc gtc gtc ggc atc tcc agc gat ctg ctc tac			864
Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr			
275	280	285	
ccc gcc gcc gag gtc cgc gcc tgc gcc gcc gag ctt ccc cac gcc gac			912
Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp			
290	295	300	
tac tgg gaa ctg ggc agc att cac ggc cac gac gcc ttt ttg atg gac			960
Tyr Trp Glu Leu Gly Ser Ile His Gly His Asp Ala Phe Leu Met Asp			
305	310	315	320
cca cag gac ttg ccg gag cgg gtg ggg gcg ttt ctc agg agt			1002
Pro Gln Asp Leu Pro Glu Arg Val Gly Ala Phe Leu Arg Ser			
325	330		
tga			1005

<210> 30
<211> 334
<212> PRT
<213> Deinococcus radiodurans

<400> 30

Val Thr Ala Val Leu Ala Gly His Ala Ser Ala Leu Leu Leu Thr Glu
 1 5 10 15

Glu Pro Asp Cys Ser Gly Pro Gln Thr Val Val Leu Phe Arg Arg Glu
 20 25 30

Pro Leu Leu Leu Asp Cys Gly Arg Ala Leu Ser Asp Val Arg Val Ala
 35 40 45

Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His
 50 55 60

Ala Leu Thr Gly Asp Ser Ala Val His Glu Trp Trp Pro Asp Phe Leu
 65 70 75 80

Gly Ala Gly Arg Pro Leu Asp Pro Ala Asp Asp Tyr Val Val Cys Ala
 85 90 95

Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala
 100 105 110

Ala Thr Cys Ser Gly Pro Val Pro Leu Ser Leu Arg Asp Met Ala Arg
 115 120 125

Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val
 130 135 140

Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu
 145 150 155 160

Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg
 165 170 175

His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile
 180 185 190

Ala Leu Ala Pro Gly Gly Glu Gly Leu Lys Val Ala Arg Gln Ile Ala
 195 200 205

Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly
 210 215 220

Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln
 225 230 235 240

Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu
 245 250 255

Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala
 260 265 270

Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr
 275 280 285

Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp
 290 295 300

Tyr Trp Glu Leu Gly Ser Ile His Gly His Asp Ala Phe Leu Met Asp
 305 310 315 320

Pro Gln Asp Leu Pro Glu Arg Val Gly Ala Phe Leu Arg Ser
 325 330

<210> 31
 <211> 1461
 <212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)...(1458)

<223> RSC08123

<400> 31

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Met	Ser	His	Thr	Leu	Lys	Ser	Lys	Thr	Leu	Gln	Glu	Leu	Asp	Ile	Glu	
1				5					10						15	

gag	att	aag	gaa	act	aac	cca	ttg	ctc	aaa	cta	gtt	caa	ggg	cag	agg	96
Glu	Ile	Lys	Glu	Thr	Asn	Pro	Leu	Leu	Lys	Leu	Val	Gln	Gly	Gln	Arg	
20							25					30				

att	gtt	caa	gtt	ccg	gaa	cta	gtg	ctt	gag	tct	ggc	gtg	gtc	ata	aat	144
Ile	Val	Gln	Val	Pro	Glu	Leu	Val	Leu	Glu	Ser	Gly	Val	Val	Ile	Asn	
35							40				45					

aat	ttc	cct	att	gct	tat	aag	acg	tgg	ggt	aca	ctg	aat	gaa	gct	ggt	192
Asn	Phe	Pro	Ile	Ala	Tyr	Lys	Thr	Trp	Gly	Thr	Leu	Asn	Glu	Ala	Gly	
50							55				60					

gat	aat	gtt	ctg	gta	att	tgt	cat	gcc	ttg	act	ggg	tcc	gca	gat	gtt	240
Asp	Asn	Val	Leu	Val	Ile	Cys	His	Ala	Leu	Thr	Gly	Ser	Ala	Asp	Val	
65							70			75		80				

gct	gac	tgg	tgg	ggc	cct	ctt	ctg	ggt	aac	gac	tta	gca	ttc	gac	cca	288
Ala	Asp	Trp	Trp	Gly	Pro	Leu	Leu	Gly	Asn	Asp	Leu	Ala	Phe	Asp	Pro	
							85			90		95				

tca	agg	ttt	ttt	atc	ata	tgt	tta	aac	tct	atg	ggc	tct	cca	tat	ggg	336
Ser	Arg	Phe	Ile	Ile	Cys	Leu	Asn	Ser	Met	Gly	Ser	Pro	Tyr	Gly		
100							105				110					

tct	ttt	tcg	cca	tta	acg	ata	aat	gag	gag	acg	ggc	gtt	aga	tat	gga	384
Ser	Phe	Ser	Pro	Leu	Thr	Ile	Asn	Glu	Glu	Thr	Gly	Val	Arg	Tyr	Gly	
115							120				125					

ccc	gaa	ttc	cca	tta	tgt	act	gtg	cgc	gat	gac	gtt	aga	gct	cac	aga	432
Pro	Glu	Phe	Pro	Leu	Cys	Thr	Val	Arg	Asp	Asp	Val	Arg	Ala	His	Arg	
130							135				140					

att	gtt	ctg	gat	tct	ctg	gga	gta	aag	tca	ata	gcc	tgt	gtt	att	ggt	480
Ile	Val	Leu	Asp	Ser	Leu	Gly	Val	Lys	Ser	Ile	Ala	Cys	Val	Ile	Gly	
145							150			155		160				

ggc	tct	atg	ggg	ggg	atg	ctg	agt	ttg	gaa	tgg	gct	gcc	atg	tat	ggt	528
Gly	Ser	Met	Gly	Gly	Met	Leu	Ser	Leu	Glu	Trp	Ala	Ala	Met	Tyr	Gly	
165							170				175					

aag	gaa	tat	gtg	aag	aat	atg	gtt	gct	ctg	gcg	aca	tca	gca	aga	cat	576
Lys	Glu	Tyr	Val	Lys	Asn	Met	Val	Ala	Leu	Ala	Thr	Ser	Ala	Arg	His	
180							185				190					

tct	gcc	tgg	tgc	ata	tcg	tgg	tct	gag	gct	caa	aga	caa	tcg	att	tac	624
Ser	Ala	Trp	Cys	Ile	Ser	Trp	Ser	Glu	Ala	Gln	Arg	Gln	Ser	Ile	Tyr	
195							200				205					

tca	gat	ccc	aac	tac	ttg	gac	ggg	tac	tat	ccg	gta	gag	gag	caa	cct	672
Ser	Asp	Pro	Asn	Tyr	Leu	Asp	Gly	Tyr	Tyr	Pro	Val	Glu	Glu	Gln	Pro	
210							215				220					

gtg	gcc	gga	cta	tcg	gct	gca	cgt	atg	tct	gca	ttg	ttg	acg	tac	agg	720
Val	Ala	Gly	Leu	Ser	Ala	Ala	Arg	Met	Ser	Ala	Leu	Leu	Thr	Tyr	Arg	
225							230				235			240		

aca aga aac agt ttc gag aac aaa ttc tcc aga aga tct cct tca ata	768
Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile	
245 250 255	
gca caa caa caa aaa gct caa agg gag gag aca cgc aaa cca tct act	816
Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr	
260 265 270	
gtc agc gaa cac tcc cta caa atc cac aat gat ggg tat aaa aca aaa	864
Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys	
275 280 285	
gcc agc act gcc atc gct ggc att tct ggg caa aaa ggt caa agc gtg	912
Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val	
290 295 300	
gtg tcc acc gca tct tct tcg gat tca ttg aat tct tca aca tcg atg	960
Val Ser Thr Ala Ser Ser Asp Ser Leu Asn Ser Thr Ser Met	
305 310 315 320	
act tcg gta agt tct gta acg ggt gaa gtg aag gac ata aag cct gcg	1008
Thr Ser Val Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala	
325 330 335	
cag acg tat ttt tct gca caa agt tac ttg agg tac cag ggc aca aag	1056
Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys	
340 345 350	
ttc atc aat agg ttc gac gcc aat tgt tac att gcc atc aca cgt aaa	1104
Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys	
355 360 365	
ctg gat acg cac gat ttg gca aga gac aga gta gat gac atc act gag	1152
Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu	
370 375 380	
gtc ctt tct acc atc caa caa cca tcc ctg atc atc ggt atc caa tct	1200
Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser	
385 390 395 400	
gat gga ctg ttc aca tat tca gaa caa gaa ttt ttg gct gag cac ata	1248
Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile	
405 410 415	
ccg aag tcg caa tta gaa aaa att gaa tct ccc gaa ggc cac gat gcc	1296
Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala	
420 425 430	
ttc cta ttg gag ttt aag ctg ata aac aaa ctg ata gta caa ttt tta	1344
Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu	
435 440 445	
aaa acc aac tgc aag gcc att acc gat gcc gct cca aga gct tgg gga	1392
Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly	
450 455 460	
ggt gac gtt ggt aac gat gaa acg aag acg tct gtc ttt ggt gag gcc	1440
Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala	
465 470 475 480	
gaa gaa gtt acc aac tgg tag	1461
Glu Glu Val Thr Asn Trp	
485	

<211> 486
 <212> PRT
 <213> *Saccharomyces cerevisiae*

 <400> 32
 Met Ser His Thr Leu Lys Ser Lys Thr Leu Gln Glu Leu Asp Ile Glu
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 Glu Ile Lys Glu Thr Asn Pro Leu Leu Lys Leu Val Gln Gly Gln Arg
 20 25 30

 Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
 35 40 45

 Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
 50 55 60

 Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
 65 70 75 80

 Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
 85 90 95

 Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
 100 105 110

 Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
 115 120 125

 Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg
 130 135 140

 Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly
 145 150 155 160

 Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly
 165 170 175

 Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His
 180 185 190

 Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr
 195 200 205

 Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro
 210 215 220

 Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg
 225 230 235 240

 Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile
 245 250 255

 Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr
 260 265 270

 Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys
 275 280 285

 Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val
 290 295 300

 Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met
 305 310 315 320

 Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala
 325 330 335

Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys
 340 345 350
 Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys
 355 360 365
 Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu
 370 375 380
 Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser
 385 390 395 400
 Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile
 405 410 415
 Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala
 420 425 430
 Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu
 435 440 445
 Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly
 450 455 460
 Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala
 465 470 475 480
 Glu Glu Val Thr Asn Trp
 485

<210> 33
 <211> 1470
 <212> DNA
 <213> Schizosaccharomyces pombe

<220>
 <221> CDS
 <222> (1)...(1467)
 <223> RSO01936

<400> 33
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 Met Glu Ser Gln Ser Pro Ile Glu Ser Ile Val Phe Thr Asp Ser Cys
 1 5 10 15
 cat ccg tct cag caa gaa aat aaa ttt gtt cag ctt att tca gat caa 96
 His Pro Ser Gln Gln Glu Asn Lys Phe Val Gln Leu Ile Ser Asp Gln
 20 25 30
 aaa att gca att gtt ccc aaa ttt acg ttg gag tgt ggc gac atc ctt 144
 Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu
 35 40 45
 tac gat gtt ccc gtt gcc ttc aag act tgg ggt act ttg aat aaa gaa 192
 Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu
 50 55 60
 gga aac aat tgt ctt ctt tgt cat gct tta agt ggt tct gct gat 240
 Gly Asn Asn Cys Leu Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp
 65 70 75 80
 gct gga gat tgg tgg ggt cct tta ctc ggt cct ggt cgt gcg ttt gat 288
 Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp
 85 90 95

cca tca cat ttc ttt atc gta tgc ctt aat tct ctt ggt agc cca tac Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr 100 105 110	336
gga agc gcc tct cct gtt aca tgg aac gct gag act cat agt gtt tat Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr 115 120 125	384
ggg cca gaa ttt cct tta gca acc ata cgt gat gat gta aac atc cat Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His 130 135 140	432
aaa ctt att tta caa aga ttg ggt gta aag caa att gct atg gca gta Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val 145 150 155 160	480
ggt ggc tcc atg ggt ggt atg ctg gtt ttg gag tgg gca ttt gat aag Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys 165 170 175	528
gaa ttt gtg cga tca att gtt ccc att tct acc tct ctt cgt cat tcc Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser 180 185 190	576
gcg tgg tgc att agc tgg tct gaa gcg caa cgc cag agt ata tat tct Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser 195 200 205	624
gac cct aag ttt aat gat gga tac tac ggc ata gac gat cag cct gta Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val 210 215 220	672
agt ggc ctt gga gct gct cgt atg tct gcc ttg aca tat cgc tcc Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser 225 230 235 240	720
aaa tgt tct ttc gaa cgt cgc ttt gcc cgt act gtt cct gat gcg tct Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser 245 250 255	768
cgt cac ccc tat cca gat cgt tta ccc act cct ctc acg ccc agt aat Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn 260 265 270	816
gca cat tgg gtc gtt cac aac gaa gga aac cgt aat cgc cgt gaa cga Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Glu Arg 275 280 285	864
cct tgt cga tcc aat gga tca tca cct act tct gaa agt gct tta aat Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn 290 295 300	912
tcc ccc gcc tct tct gtc tcg tct tta cct tct tta ggt gcc tct cag Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln 305 310 315 320	960
act aca gac agt tct tcc ctt aac cag agt tcg tta tta aga cgt cct Thr Thr Asp Ser Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro 325 330 335	1008
gct aat act tac ttc tct gcg caa tcg tat tta cgt tac caa gcg aag Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys 340 345 350	1056
aag ttt gta agt cgc ttt gat gct aat tgt tac att tcg att act aaa Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys 355 360 365	1104

aag ttg gac acc cat gat att act cgt gga cgc ggt tca gac tct cct		1152
Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro		
370 375 380		
aag gaa gtc atg aag gat ttg tct tta ccc gta ctc gta ctc ggt att		1200
Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile		
385 390 395 400		
gaa agc gat ggt ctt ttc aca ttt gac gaa caa gtt gaa att gcc aaa		1248
Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys		
405 410 415		
tct ttt ccc aat gct acc ttg gaa aaa att att tcg gcc gaa ggc cac		1296
Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His		
420 425 430		
gac ggt ttt ttg ctt gag ttt act caa gta aac tca cat att caa aaa		1344
Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys		
435 440 445		
ttc caa aag gaa cat tta att gat atc atg tct caa act aat tcc ttt		1392
Phe Gln Lys Glu His Leu Ile Asp Ile Met Ser Gln Thr Asn Ser Phe		
450 455 460		
gag cga ctt gat tcc caa gtt aat gat acc aac cgc gaa agc gtt ttt		1440
Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe		
465 470 475 480		
gga gaa atg gaa gac ata acc tcc tgg taa		1470
Gly Glu Met Glu Asp Ile Thr Ser Trp		
485		

<210> 34
<211> 489
<212> PRT
<213> Schizosaccharomyces pombe

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His Pro Ser Gln Gln Glu Asn Lys Phe Val Gln Leu Ile Ser Asp Gln		
20 25 30		
Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu		
35 40 45		
Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu		
50 55 60		
Gly Asn Asn Cys Leu Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp		
65 70 75 80		
Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp		
85 90 95		
Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr		
100 105 110		
Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr		
115 120 125		
Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His		
130 135 140		

Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val
 145 150 155 160
 Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys
 165 170 175
 Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser
 180 185 190
 Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser
 195 200 205
 Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val
 210 215 220
 Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser
 225 230 235 240
 Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser
 245 250 255
 Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn
 260 265 270
 Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Arg Glu Arg
 275 280 285
 Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn
 290 295 300
 Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln
 305 310 315 320
 Thr Thr Asp Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro
 325 330 335
 Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys
 340 345 350
 Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys
 355 360 365
 Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro
 370 375 380
 Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile
 385 390 395 400
 Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys
 405 410 415
 Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His
 420 425 430
 Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys
 435 440 445
 Phe Gln Lys Glu His Leu Ile Asp Ile Met Ser Gln Thr Asn Ser Phe
 450 455 460
 Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe
 465 470 475 480
 Gly Glu Met Glu Asp Ile Thr Ser Trp
 485

<210> 35
 <211> 1113
 <212> DNA
 <213> Xylella almond

 <220>
 <221> CDS
 <222> (1)..(1110)
 <223> RXFX01562

 <400> 35
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 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
 1 5 10 15

 cca ttt gcg atg aag cgt ggc gga caa ctc cac cac gcc cgc atc gct 96
 Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30

 tac gaa aca tgg ggc cgc ctc aat gcc agc gcc acc aat gcc att ctg 144
 Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45

 atc atg cct ggc tta tca ccc aat gca cat gcc gca cac cat gac agc 192
 Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60

 aat gct gag cca ggc tgg tgg gag tca atg cta ggt cca ggc aaa ccc 240
 Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80

 atc gac aca gac cgt tgg ttc gtg atc tgt gtc aac tca ctt ggt agc 288
 Ile Asp Thr Asp Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95

 tgc aaa gga tcg act ggc cct gca tcg tac aac ccc atc acg cag gcc 336
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110

 atg tat cgt ttg gac ttt cca gca ctg tca atc gaa gac ggg gcc aac 384
 Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125

 tcc gca att gaa gtg gta cat gca ctg ggc atc aag caa ctt gcc agc 432
 Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140

 ctg atc ggc aat tca atg ggc ggc atg acg gca ctg gcc atc ctg ctg 480
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu
 145 150 155 160

 tta cat cca gat ata gcc cgc agc cac atc aac atc tca ggc agc gcg 528
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175

 cag gca tta ccg ttt tcc atc gcc att cgc tcg cta caa cgc gag gcg 576
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190

 atc cgc ctg gac ccc cat tgg agg cag gga gac tac gac gac acc cac 624
 Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205

 tac ccg gaa tcg ggg cta cgc atc gca cgc aaa ctt ggg gtg atc acc 672
 Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220

tac cgc tcc gcg ctg gaa tgg gac ggg cgt ttt ggc cgg gta cgc ttg Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu 225 230 235 240	720
gat tcg gac caa acc aac gac aca cca ttc gga ctg gaa ttc caa att Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile 245 250 255	768
gaa aac tac ttg gaa agc cat gca cac cgc ttc gtg cac acc ttc gac Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp 260 265 270	816
cca aac tgc tac ctg tac ctg agc cgc tcc atg gac tgg ttc gac gtg Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val 275 280 285	864
gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg 290 295 300	912
atc caa cgc gca ctc gcc atc ggt agc cat acc gac atc ctc ttt cca Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro 305 310 315 320	960
ata caa cag caa caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca Ile Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Thr 325 330 335	1008
cac gcc acc ttc ctg ggc ctt gac tca ccg cag ggg cat gat gcg ttc His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe 340 345 350	1056
ctt gtg gat atc gca aga ttt ggc cct cca gtg aag gaa ttt ctg gac Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp 355 360 365	1104
gaa ctg tga Glu Leu 370	1113

<210> 36
<211> 370
<212> PRT
<213> Xylella almond

<400> 36 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser 1 5 10 15
Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala 20 25 30
Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu 35 40 45
Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser 50 55 60
Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro 65 70 75 80
Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser 85 90 95
Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala 100 105 110

Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125
 Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu
 145 150 155 160
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190
 Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205
 Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220
 Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240
 Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 245 250 255
 Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270
 Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285
 Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300
 Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320
 Ile Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335
 His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350
 Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp
 355 360 365
 Glu Leu
 370

<210> 37
 <211> 1113
 <212> DNA
 <213> Xylella oleander

<220>
 <221> CDS
 <222> (1)...(1110)
 <223> RXYFY01729

<400> 37
 atg acc gaa ttt atc cct ccg ggc agc cta ttc cat gcg ctc tcc tct 48
 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
 1 5 10 15

cca ttt gcg atg aag cgt ggc gga caa ctc cac cac gcc cgcc atc gct		96	
Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala			
20	25	30	
tac gaa aca tgg ggc cgc ctc aat gcc agc gcc acc aat gcc att ctg		144	
Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu			
35	40	45	
atc atg cct ggc tta tca ccc aat gca cat gcc gca cac cat gac agc		192	
Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser			
50	55	60	
aat gct gag cca ggc tgg tgg gag tca atg cta ggt cca ggc aaa ccc		240	
Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro			
65	70	75	80
atc gac aca gac cgt tgg ttc gtg atc tgt gtc aac tca ctt ggt agc		288	
Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser			
85	90	95	
tgc aaa gga tcg act ggc cct gca tcg tac aac ccc atc acg cag gcc		336	
Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala			
100	105	110	
atg tat cgt ttg gac ttt cca gca ctg tca atc gaa gac ggg gcc aac		384	
Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn			
115	120	125	
gcc gca att gaa gtg gta cat gca ctg ggc atc aag caa ctt gcc agc		432	
Ala Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser			
130	135	140	
ctg atc ggc aat tca atg ggg ggc atg acg aca ctg gcc atc ctg ctg		480	
Leu Ile Gly Asn Ser Met Gly Gly Met Thr Thr Leu Ala Ile Leu Leu			
145	150	155	160
tta cat cca gat att gcc cgc agc cac atc aac atc tca ggc agc gcg		528	
Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala			
165	170	175	
cag gca tta ccg ttt tcc atc gcc att cgc tcg cta caa cgc gag gcg		576	
Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala			
180	185	190	
atc cgc ctg gac ccc cat tgg aag cag gga gac tac gac gac acc cac		624	
Ile Arg Leu Asp Pro His Trp Lys Gln Gly Asp Tyr Asp Asp Thr His			
195	200	205	
tac ccg gaa tcg ggg cta cgc atc gca cgc aaa ctc ggg gtg atc acc		672	
Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr			
210	215	220	
tac cgc tcc gcg ctg gaa tgg gac ggg cgt ttt ggc cgg gta cgc ttg		720	
Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu			
225	230	235	240
gat tcg gac caa acc aac gac aca cca ttc gga ctg gaa ttc caa att		768	
Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile			
245	250	255	
gaa aac tac ttg gaa agc cat gca cac cgc ttc gtg cac acc ttc gac		816	
Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp			
260	265	270	
cca aac tgc tac ctg tac agc cgc tcc atg gac tgg ttc gac gtg		864	
Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val			

275

280

285

gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga 912
 Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300

atc caa cgc gca ctt gcc atc ggt agc cat acc gac atc ctc ttt cca 960
 Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320

ata caa cag caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca 1008
 Ile Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Thr
 325 330 335

cac gcc acc ttc ctg ggc ctt gac tca ccg cag gga cat gat gcg ttc 1056
 His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350

ctt gtg gat atc gca gga ttt ggc cct cca gtg aag gaa ttt ctg ggc 1104
 Leu Val Asp Ile Ala Gly Phe Gly Pro Pro Val Lys Glu Phe Leu Gly
 355 360 365

gaa ctg tga 1113
 Glu Leu
 370

<210> 38

<211> 370

<212> PRT

<213> Xylella oleander

<400> 38

Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
 1 5 10 15

Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30

Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45

Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60

Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80

Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95

Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110

Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125

Ala Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140

Leu Ile Gly Asn Ser Met Gly Gly Met Thr Thr Leu Ala Ile Leu Leu
 145 150 155 160

Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175

Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala

180	185	190
Ile Arg Leu Asp Pro His Trp Lys Gln Gly Asp Tyr Asp Asp Thr His 195	200	205
Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr 210	215	220
Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu 225	230	235
Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile 245	250	255
Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp 260	265	270
Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val 275	280	285
Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg 290	295	300
Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro 305	310	315
Ile Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr 325	330	335
His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe 340	345	350
Leu Val Asp Ile Ala Gly Phe Gly Pro Pro Val Lys Glu Phe Leu Gly 355	360	365
Glu Leu 370		

<210> 39
<211> 1578
<212> DNA
<213> *Emericella nidulans*

<220>
<221> CDS
<222> (1)...(1575)
<223> REN00010

<400> 39				
atg agt ccg ctg aac ggc gtc gct cgt tcc ttt ccg cgg ccc ttc cag Met Ser Pro Leu Asn Gly Val Ala Arg Ser Phe Pro Arg Pro Phe Gln	1	5	10	48
				15
gcc gtg acc agg cgg cct ttt cga gtt gtc cag ccg gcc atc gcc tgt Ala Val Thr Arg Arg Pro Phe Arg Val Val Gln Pro Ala Ile Ala Cys	20	25	30	96
ccg tcc aac agc cgg tcg ttt aac cat tct cga tca tta cga tca acg Pro Ser Asn Ser Arg Ser Phe Asn His Ser Arg Ser Leu Arg Ser Thr	35	40	45	144
ggg tct cag tcc ccc gct cca tcc cca cgc gac tcc tcg aat ccc gcg Gly Ser Gln Ser Pro Ala Pro Ser Pro Arg Asp Ser Ser Asn Pro Ala	50	55	60	192
ctg tcc ttc cct tgc ctc gac gcc cag gag gcc aag tcc gct ctt ctt				240

Leu Ser Phe Pro Cys Leu Asp Ala Gln Glu Ala Lys Ser Ala Leu Leu			
65	70	75	80
tcc gcg cga tct ctt ggt tca ggc cct gaa ccc tcc tat acc gcc ggc			288
Ser Ala Arg Ser Leu Gly Ser Gly Pro Glu Pro Ser Tyr Thr Ala Gly			
85	90	95	
cac cac gaa cga ttc cat tcc gac gaa ccg ctg ctc ctt gat tgg ggc			336
His His Glu Arg Phe His Ser Asp Glu Pro Leu Leu Leu Asp Trp Gly			
100	105	110	
ggt ttg ctt cca gaa ttt gat atc gca tat gag aca tgg ggc cag ctg			384
Gly Leu Leu Pro Glu Phe Asp Ile Ala Tyr Glu Thr Trp Gly Gln Leu			
115	120	125	
aac gag aag aag gat aat gtc att ctg ctg cat acc ggt ctg tct gca			432
Asn Glu Lys Lys Asp Asn Val Ile Leu Leu His Thr Gly Leu Ser Ala			
130	135	140	
tct agc cat gcg cac agc acc gaa gcg aac ccg aag ccc ggc tgg tgg			480
Ser Ser His Ala His Ser Thr Glu Ala Asn Pro Lys Pro Gly Trp Trp			
145	150	155	160
gag aaa ttc ata ggt cct ggg aag acg cta gat acg gac aag tac ttt			528
Glu Lys Phe Ile Gly Pro Gly Lys Thr Leu Asp Thr Asp Lys Tyr Phe			
165	170	175	
gtg atc tgc acc aat gtc ctt gga ggg tgc tac ggt agc acg ggg ccc			576
Val Ile Cys Thr Asn Val Leu Gly Gly Cys Tyr Gly Ser Thr Gly Pro			
180	185	190	
tgc acg gtg gac ccg tcg gat ggg aag aag tat gct acg cgg ttt ccc			624
Ser Thr Val Asp Pro Ser Asp Gly Lys Lys Tyr Ala Thr Arg Phe Pro			
195	200	205	
atc ctg aca att gaa gat atg gtg cga gcg cag ttc cgc ctt ttg gac			672
Ile Leu Thr Ile Glu Asp Met Val Arg Ala Gln Phe Arg Leu Leu Asp			
210	215	220	
cat ctt ggg gtt cgg aaa ctc tac gcg tcc gtc ggc tcc agc atg ggt			720
His Leu Gly Val Arg Lys Leu Tyr Ala Ser Val Gly Ser Ser Met Gly			
225	230	235	240
ggt atg cag agt ctt gca gcc ggt gtt ctg ttc cca gag cga gtg ggc			768
Gly Met Gln Ser Leu Ala Ala Gly Val Leu Phe Pro Glu Arg Val Gly			
245	250	255	
aag att gtg tcg att agc ggt tgt gct cga agc cat ccg tac agc att			816
Lys Ile Val Ser Ile Ser Gly Cys Ala Arg Ser His Pro Tyr Ser Ile			
260	265	270	
gct atg cgc cat acc cag ccg cag gtg ttg atg atg gat cca aat tgg			864
Ala Met Arg His Thr Gln Arg Gln Val Leu Met Met Asp Pro Asn Trp			
275	280	285	
gct cga ggt ttc tac tac gat tcg atc cca cct cat tca ggc atg aag			912
Ala Arg Gly Phe Tyr Tyr Asp Ser Ile Pro Pro His Ser Gly Met Lys			
290	295	300	
ctc gct cgc gag att gcc acc gtc acg tac cgc agc gga cca gaa tgg			960
Leu Ala Arg Glu Ile Ala Thr Val Thr Tyr Arg Ser Gly Pro Glu Trp			
305	310	315	320
gag aaa cgc ttt ggt cgg aaa cgg gct gat ccg agc aaa cag cct gcg			1008
Glu Lys Arg Phe Gly Arg Lys Arg Ala Asp Pro Ser Lys Gln Pro Ala			
325	330	335	

ctt tgc ccc gac ttt ctc atc gag acg tat ctc gac cac gcc ggt gaa Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu 340 345 350	1056
aaa ttc tgc ttg gaa tac gat gcc aac agc ctg ctc tac atc tcc aag Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys 355 360 365	1104
gcg atg gat ctg ttt gac cta ggg ttg act cag caa ctc gcg acg aag Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys 370 375 380	1152
aag cag agg gcg gag gcc cag gcg aag att agc agc gga aca aac act Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr 385 390 395 400	1200
gtc aat gat gcg tcg tgc agc ctt aca ctt cct gaa cag cca tac cag Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln 405 410 415	1248
gag cag cca tct gcc tcg aca tcc gcc gag cag tct gct tcc gct tca Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser 420 425 430	1296
gag acc ggg tcg gct ccg aac gat ctt gtt gcc ggg ctt gcg ccg ctg Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu 435 440 445	1344
aaa gac cat cag gtg ctg gta atc gga gtc gca agc gac att ctc ttc Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe 450 455 460	1392
ccg gcg tgg caa cag cgc gag atc gcg gag act ctg att caa gca ggg Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly 465 470 475 480	1440
aac aag acc gtg gag cat att gag ctg ggc aac gac gtg tct ctc ttt Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe 485 490 495	1488
ggt cat gac aca ttc ctc ctt gat gtc aga acg tcg gag gcg cag ttc Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe 500 505 510	1536
gca agt tcc gta cta gtc ggc tcg cac ata att gta caa tag Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln 515 520 525	1578
<210> 40	
<211> 525	
<212> PRT	
<213> Emericella nidulans	
<400> 40	
Met Ser Pro Leu Asn Gly Val Ala Arg Ser Phe Pro Arg Pro Phe Gln 1 5 10 15	
Ala Val Thr Arg Arg Pro Phe Arg Val Val Gln Pro Ala Ile Ala Cys 20 25 30	
Pro Ser Asn Ser Arg Ser Phe Asn His Ser Arg Ser Leu Arg Ser Thr 35 40 45	
Gly Ser Gln Ser Pro Ala Pro Ser Pro Arg Asp Ser Ser Asn Pro Ala 50 55 60	

Leu Ser Phe Pro Cys Leu Asp Ala Gln Glu Ala Lys Ser Ala Leu Leu
 65 70 75 80
 Ser Ala Arg Ser Leu Gly Ser Gly Pro Glu Pro Ser Tyr Thr Ala Gly
 85 90 95
 His His Glu Arg Phe His Ser Asp Glu Pro Leu Leu Leu Asp Trp Gly
 100 105 110
 Gly Leu Leu Pro Glu Phe Asp Ile Ala Tyr Glu Thr Trp Gly Gln Leu
 115 120 125
 Asn Glu Lys Lys Asp Asn Val Ile Leu Leu His Thr Gly Leu Ser Ala
 130 135 140
 Ser Ser His Ala His Ser Thr Glu Ala Asn Pro Lys Pro Gly Trp Trp
 145 150 155 160
 Glu Lys Phe Ile Gly Pro Gly Lys Thr Leu Asp Thr Asp Lys Tyr Phe
 165 170 175
 Val Ile Cys Thr Asn Val Leu Gly Gly Cys Tyr Gly Ser Thr Gly Pro
 180 185 190
 Ser Thr Val Asp Pro Ser Asp Gly Lys Lys Tyr Ala Thr Arg Phe Pro
 195 200 205
 Ile Leu Thr Ile Glu Asp Met Val Arg Ala Gln Phe Arg Leu Leu Asp
 210 215 220
 His Leu Gly Val Arg Lys Leu Tyr Ala Ser Val Gly Ser Ser Met Gly
 225 230 235 240
 Gly Met Gln Ser Leu Ala Ala Gly Val Leu Phe Pro Glu Arg Val Gly
 245 250 255
 Lys Ile Val Ser Ile Ser Gly Cys Ala Arg Ser His Pro Tyr Ser Ile
 260 265 270
 Ala Met Arg His Thr Gln Arg Gln Val Leu Met Met Asp Pro Asn Trp
 275 280 285
 Ala Arg Gly Phe Tyr Tyr Asp Ser Ile Pro Pro His Ser Gly Met Lys
 290 295 300
 Leu Ala Arg Glu Ile Ala Thr Val Thr Tyr Arg Ser Gly Pro Glu Trp
 305 310 315 320
 Glu Lys Arg Phe Gly Arg Lys Arg Ala Asp Pro Ser Lys Gln Pro Ala
 325 330 335
 Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu
 340 345 350
 Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys
 355 360 365
 Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys
 370 375 380
 Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr
 385 390 395 400
 Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln
 405 410 415
 Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser

420 425 430

Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu
 435 440 445

Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe
 450 455 460

Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly
 465 470 475 480

Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe
 485 490 495

Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe
 500 505 510

Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln
 515 520 525

<210> 41

<211> 1170

<212> DNA

<213> Mesorhizobium loti

<220>

<221> CDS

<222> (1)...(1167)

<223> NP_104621

<400> 41

atg	gcc	gct	ctg	cgc	gca	gga	aag	acc	aac	aac	gag	gcc	gac	cag	ccg		48
Met	Ala	Ala	Leu	Arg	Ala	Gly	Lys	Thr	Asn	Asn	Glu	Ala	Asp	Gln	Pro		
1			5					10							15		

tcg	agc	ccg	gtg	ttg	cgc	tgc	ggg	gcg	gac	aag	ccg	ctc	aag	ctc	gac		96
Ser	Ser	Pro	Val	Leu	Arg	Phe	Gly	Ala	Asp	Lys	Pro	Leu	Lys	Leu	Asp		
20				25											30		

gcc	ggc	acg	ctt	ttg	tcg	ccg	ttc	cag	atc	gcc	tat	cag	acc	tac	ggc		144
Ala	Gly	Thr	Leu	Leu	Ser	Pro	Phe	Gln	Ile	Ala	Tyr	Gln	Thr	Tyr	Gly		
35					40										45		

acg	ctg	aac	gat	gcc	cgc	tcc	aat	gcc	atc	ctc	gtc	tgc	cat	gcf	ctg		192
Thr	Ieu	Asn	Asp	Ala	Arg	Ser	Asn	Ala	Ile	Leu	Val	Cys	His	Ala	Ieu		
50					55										60		

acc	ggc	gac	cag	cat	gtc	gcc	aac	acc	aat	ccg	gtg	acc	ggc	aag	ccg		240
Thr	Gly	Asp	Gln	His	Val	Ala	Asn	Thr	Asn	Pro	Val	Thr	Gly	Lys	Pro		
65					70										80		

gga	tgg	tgg	gaa	gtg	ctg	atc	ggc	ccc	ggc	agg	atc	atc	gac	acc	aac		288
Gly	Trp	Trp	Glu	Val	Leu	Ile	Gly	Pro	Gly	Arg	Ile	Ile	Asp	Thr	Asn		
85					90										95		

cgt	ttc	ttc	gtc	atc	tgc	tcc	aac	gtc	atc	ggc	ggt	tgt	ctg	ggc	tcc		336
Arg	Phe	Phe	Val	Ile	Cys	Ser	Asn	Val	Ile	Gly	Gly	Cys	Leu	Gly	Ser		
100					105										110		

acc	ggc	ccg	gcc	tcg	acc	aac	ccc	gcc	acc	ggc	aag	ccc	tac	ggg	ctc		384
Thr	Gly	Pro	Ala	Ser	Thr	Asn	Pro	Ala	Thr	Gly	Lys	Pro	Tyr	Gly	Leu		
115						120									125		

gac	ctg	ccg	gtc	atc	acc	atc	cgc	gat	atg	gtg	cgc	gag	cag	cag	atg		432
Asp	Leu	Pro	Val	Ile	Thr	Ile	Arg	Asp	Met	Val	Arg	Ala	Gln	Gln	Met		
130					135										140		

ctg atc gat cat ttc ggc atc gag aaa ctg ttc tgc gtc ctc ggc ggc Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly 145 150 155 160	480
tcg atg ggc gga atg cag gtg ctg gaa tgg gcg tcg agc tac ccc gag Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu 165 170 175	528
cgc gtc ttt tcg gca ctg ccg atc gcc acc ggc gcg cgc cat tcc tcg Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser 180 185 190	576
cag aac atc gcc ttc cac gag gtc ggc cgg cag gct gtc atg gcc gat Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp 195 200 205	624
ccg gac tgg cac ggc ggc aaa tat ttc gaa aac ggc aaa cgc ccg gaa Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu 210 215 220	672
aag ggc ctg gcg gta gcg ccg atg gcc cac ata acc tat ctg tcg Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser 225 230 235 240	720
gaa gcc gcc ctg cac ccg aaa ttc ggc cgc aat ctg cag gat cgc gag Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu 245 250 255	768
gcg ctg acc ttc ggc ttc gac gcc gac ttc cag atc gaa agc tat ctg Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu 260 265 270	816
cgc cac caa ggc atg acc ttc gtc gac cgc ttc gac gcc aat tcc tat Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr 275 280 285	864
ctc tac atg acg ccg tcg atg gac tat ttc gac ctc gcc gcc gat cat Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His 290 295 300	912
ggc ggg ccg ctg gcg gat gcc ttt gcc ggc acc aaa acc cgc ttc tgc Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys 305 310 315 320	960
ctg gtg tcc ttc acc tcg gat tgg ttg ttt ccg acc gaa gag agc cgc Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg 325 330 335	1008
tcg atc gtg cac gcg ctc aac gcc gcc ggc gcg tcc gtg tcc ttc gtc Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val 340 345 350	1056
gaa atc gag acc gac cgc ggc cac gat gcc ttc ctg ctc gac gag ccg Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro 355 360 365	1104
gaa ctg ttc gcc gcc atc aac ggc ttc atc ggc tcc gcg gcg cgg gcg Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala 370 375 380	1152
aga ggg cta agc gca tga Arg Gly Leu Ser Ala 385	1170

<211> 389

<212> PRT

<213> Mesorhizobium loti

<400> 42

Met Ala Ala Leu Arg Ala Gly Lys Thr Asn Asn Glu Ala Asp Gln Pro			
1	5	10	15

Ser Ser Pro Val Leu Arg Phe Gly Ala Asp Lys Pro Leu Lys Leu Asp		
20	25	30

Ala Gly Thr Leu Leu Ser Pro Phe Gln Ile Ala Tyr Gln Thr Tyr Gly		
35	40	45

Thr Leu Asn Asp Ala Arg Ser Asn Ala Ile Leu Val Cys His Ala Leu		
50	55	60

Thr Gly Asp Gln His Val Ala Asn Thr Asn Pro Val Thr Gly Lys Pro			
65	70	75	80

Gly Trp Trp Glu Val Leu Ile Gly Pro Gly Arg Ile Ile Asp Thr Asn		
85	90	95

Arg Phe Phe Val Ile Cys Ser Asn Val Ile Gly Gly Cys Leu Gly Ser		
100	105	110

Thr Gly Pro Ala Ser Thr Asn Pro Ala Thr Gly Lys Pro Tyr Gly Leu		
115	120	125

Asp Leu Pro Val Ile Thr Ile Arg Asp Met Val Arg Ala Gln Gln Met		
130	135	140

Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly			
145	150	155	160

Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu		
165	170	175

Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser		
180	185	190

Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp		
195	200	205

Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu		
210	215	220

Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser			
225	230	235	240

Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu		
245	250	255

Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu		
260	265	270

Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr		
275	280	285

Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His		
290	295	300

Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys			
305	310	315	320

Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg		
325	330	335

Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val
 340 345 350

Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro
 355 360 365

Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala
 370 375 380

Arg Gly Leu Ser Ala
 385

<210> 43
<211> 1155
<212> DNA
<213> acremonium crysogenum

<220>
<221> CDS
<222> (1)..(1152)
<223> P39058

<400> 43
tgc cgc ctc aga tcg cca atc gct tcg agg ctt cgc tag atg ccc aag 48
Cys Arg Leu Arg Ser Pro Ile Ala Ser Arg Leu Arg Xaa Met Pro Lys
 1 5 10 15

aca tag cca gaa tat cgc tct tca cac tgg aat ctg gcg tca tcc ttc 96
Thr Xaa Pro Glu Tyr Arg Ser Ser His Trp Asn Leu Ala Ser Ser Phe
 20 25 30

gcg atg tac ccg tgg cat aca aat cgt ggg gtc gca tga atg tct caa 144
Ala Met Tyr Pro Trp His Thr Asn Arg Gly Val Ala Xaa Met Ser Gln
 35 40 45

ggg ata act gcg tca tcg tct gcc aca cct tga cga gca gcg ccc atg 192
Gly Ile Thr Ala Ser Ser Ala Thr Pro Xaa Arg Ala Ala Pro Met
 50 55 60

tca cct cgt ggt ggc cca cac tgt ttg gcc aag gca ggg ctt tcg ata 240
Ser Pro Arg Gly Gly Pro His Cys Leu Ala Lys Ala Gly Leu Ser Ile
 65 70 75 80

cct ctc gct act tca tca tct gcc taa att atc tcg gga gcc cct ttg 288
Pro Leu Ala Thr Ser Ser Ala Xaa Ile Ile Ser Gly Ala Pro Leu
 85 90 95

gga gtg ctg gac cat gtt cac cgg acc ccg atg cag aag gcc agc gcc 336
Gly Val Leu Asp His Val His Arg Thr Pro Met Gln Lys Ala Ser Ala
 100 105 110

cgt acg ggg cca agt ttc ctc gca cga cga ttc gag atg atg ttc gta 384
Arg Thr Gly Pro Ser Phe Leu Ala Arg Arg Phe Glu Met Met Phe Val
 115 120 125

ttc atc gcc agg tgc tcg aca ggt tag gcg tca ggc aaa ttg ctg ccg 432
Phe Ile Ala Arg Cys Ser Thr Gly Xaa Ala Ser Gly Lys Leu Leu Pro
 130 135 140

tag tcg gcg cat cca tgg gtg gaa tgc aca ctc tgg aat ggg cct tct 480
Xaa Ser Ala His Pro Trp Val Glu Cys Thr Leu Trp Asn Gly Pro Ser
 145 150 155 160

ttg gtc ccg agt acg tgc gaa aga ttg tgc cca tcg cga cat cat gcc 528
Leu Val Pro Ser Thr Cys Glu Arg Leu Cys Pro Ser Arg His His Ala

165	170	175	
gtc aga gca gct ggt gcg cag ctt ggt tcg aga cac aga ggc agt gca Val Arg Ala Ala Gly Ala Gln Leu Gly Ser Arg His Arg Gly Ser Ala 180	185	190	576
tct atg atg acc cca agt acc tgg acg ggg agt acg acg tag acg acc Ser Met Met Thr Pro Ser Thr Trp Thr Gly Ser Thr Thr Xaa Thr Thr 195	200	205	624
agc ctg tcc ggg ggc tcg aaa cag cgc gca aga ttg cga atc tca cgt Ser Leu Ser Gly Gly Ser Lys Gln Arg Ala Arg Leu Arg Ile Ser Arg 210	215	220	672
aca aga gca aac ctg cga tgg acg agc gct tcc ata tgg ctc cag gag Thr Arg Ala Asn Leu Arg Trp Thr Ser Ala Ser Ile Trp Leu Gln Glu 225	230	235	720
tcc aag ccg gcc gga ata tca gca gcc agg atg cga aga agg aaa tca Ser Lys Pro Ala Gly Ile Ser Ala Ala Arg Met Arg Arg Arg Lys Ser 245	250	255	768
acg gca cag aca gcg gca aca gcc acc gtg ctg gcc agc cca ttg aag Thr Ala Gln Thr Ala Ala Thr Ala Thr Val Leu Ala Ser Pro Leu Lys 260	265	270	816
ccg tat ctt cct atc tcc ggt acc agg ccc aga agt ttg ccg cga gct Pro Tyr Leu Pro Ile Ser Gly Thr Arg Pro Arg Ser Leu Pro Arg Ala 275	280	285	864
tcg acg cca act gct aca tcg cca tga cac tca agt tcg aca ccc acg Ser Thr Pro Thr Ala Thr Ser Pro Xaa His Ser Ser Ser Thr Pro Thr 290	295	300	912
aca tca gca gag gcc ggg cag gat caa tcc cgg agg ctc tgg caa tga Thr Ser Ala Glu Ala Gly Gln Asp Gln Ser Arg Arg Leu Trp Gln Xaa 305	310	315	960
tta cac aac cag cgt tga tca ttt gcg cca ggt cag acg gtc tgt act Leu His Asn Gln Arg Xaa Ser Phe Ala Pro Gly Gln Thr Val Cys Thr 325	330	335	1008
cgt ttg acg agc acg ttg aga tgg ggc gca gta tcc caa aca gtc gtc Arg Leu Thr Ser Thr Leu Arg Trp Gly Ala Val Ser Gln Thr Val Val 340	345	350	1056
ttt gcg tgg tgg aca cga atg agg gtc atg act tct ttg taa tgg aag Phe Ala Trp Trp Thr Arg Met Arg Val Met Thr Ser Leu Xaa Trp Lys 355	360	365	1104
cgg aca agg tta atg atg ccg tca gag gat tcc tcg atc agt cat taa Arg Thr Arg Leu Met Met Pro Ser Glu Asp Ser Ser Ile Ser His Xaa 370	375	380	1152
tgt			1155

<210> 44
<211> 384
<212> PRT
<213> acremonium crysogenum

<220>
<221> unsure
<222> 13 .. 13
<223> All occurrences of Xaa indicate any amino acid

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<220>
<221> unsure
<222> 18 .. 18
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 45 .. 45
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 59 .. 59
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 89 .. 89
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 137 .. 137
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 145 .. 145
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 206 .. 206
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 297 .. 297
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 320 .. 320
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 326 .. 326
<223> All occurrences of Xaa indicate any amino acid

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<221> unsure
<222> 366 .. 366
<223> All occurrences of Xaa indicate any amino acid

<220>
<221> unsure
<222> 384 .. 384
<223> All occurrences of Xaa indicate any amino acid

<400> 44
Cys Arg Leu Arg Ser Pro Ile Ala Ser Arg Leu Arg Xaa Met Pro Lys
    1          5          10          15

Thr Xaa Pro Glu Tyr Arg Ser Ser His Trp Asn Leu Ala Ser Ser Phe
    20         25          30

```

Ala Met Tyr Pro Trp His Thr Asn Arg Gly Val Ala Xaa Met Ser Gln
 35 40 45
 Gly Ile Thr Ala Ser Ser Ser Ala Thr Pro Xaa Arg Ala Ala Pro Met
 50 55 60
 Ser Pro Arg Gly Gly Pro His Cys Leu Ala Lys Ala Gly Leu Ser Ile
 65 70 75 80
 Pro Leu Ala Thr Ser Ser Ser Ala Xaa Ile Ile Ser Gly Ala Pro Leu
 85 90 95
 Gly Val Leu Asp His Val His Arg Thr Pro Met Gln Lys Ala Ser Ala
 100 105 110
 Arg Thr Gly Pro Ser Phe Leu Ala Arg Arg Phe Glu Met Met Phe Val
 115 120 125
 Phe Ile Ala Arg Cys Ser Thr Gly Xaa Ala Ser Gly Lys Leu Leu Pro
 130 135 140
 Xaa Ser Ala His Pro Trp Val Glu Cys Thr Leu Trp Asn Gly Pro Ser
 145 150 155 160
 Leu Val Pro Ser Thr Cys Glu Arg Leu Cys Pro Ser Arg His His Ala
 165 170 175
 Val Arg Ala Ala Gly Ala Gln Leu Gly Ser Arg His Arg Gly Ser Ala
 180 185 190
 Ser Met Met Thr Pro Ser Thr Trp Thr Gly Ser Thr Thr Xaa Thr Thr
 195 200 205
 Ser Leu Ser Gly Gly Ser Lys Gln Arg Ala Arg Leu Arg Ile Ser Arg
 210 215 220
 Thr Arg Ala Asn Leu Arg Trp Thr Ser Ala Ser Ile Trp Leu Gln Glu
 225 230 235 240
 Ser Lys Pro Ala Gly Ile Ser Ala Ala Arg Met Arg Arg Arg Lys Ser
 245 250 255
 Thr Ala Gln Thr Ala Ala Thr Ala Thr Val Leu Ala Ser Pro Leu Lys
 260 265 270
 Pro Tyr Leu Pro Ile Ser Gly Thr Arg Pro Arg Ser Leu Pro Arg Ala
 275 280 285
 Ser Thr Pro Thr Ala Thr Ser Pro Xaa His Ser Ser Ser Thr Pro Thr
 290 295 300
 Thr Ser Ala Glu Ala Gly Gln Asp Gln Ser Arg Arg Leu Trp Gln Xaa
 305 310 315 320
 Leu His Asn Gln Arg Xaa Ser Phe Ala Pro Gly Gln Thr Val Cys Thr
 325 330 335
 Arg Leu Thr Ser Thr Leu Arg Trp Gly Ala Val Ser Gln Thr Val Val
 340 345 350
 Phe Ala Trp Trp Thr Arg Met Arg Val Met Thr Ser Leu Xaa Trp Lys
 355 360 365
 Arg Thr Arg Leu Met Met Pro Ser Glu Asp Ser Ser Ile Ser His Xaa
 370 375 380

<210> 45
 <211> 1077
 <212> DNA
 <213> Pseudomonas putida

 <220>
 <221> CDS
 <222> (1)..(1074)
 <223> AAK49778

 <400> 45
 atg tca act gtc ttt ccc gaa gat tcc gtc ggt ctg gta gta cggtcaa 48
 Met Ser Thr Val Phe Pro Glu Asp Ser Val Gly Leu Val Val Arg Gln
 1 5 10 15

 acc tcc cgg ttc gat gaa ccg ctg gca ctg gcc tgt ggc cgt tca ctg 96
 Thr Ser Arg Phe Asp Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu
 20 25 30

 gcc agt tac gaa ctg gtc tac gag acc tat ggc acc ctg aac gcc agc 144
 Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser
 35 40 45

 gcg agc aac gcc gtg ctg atc tgc cat gcc ctg tcc ggc cac cac cat 192
 Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60

 gcc gct ggc tac cat gcc gcc acc gac cgc aag ccg ggc tgg tgg gac 240
 Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80

 agc tgc atc ggc ccc gga aaa ccg atc gat acc aac cgc ttc ttc gtg 288
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val
 85 90 95

 gtc agc ctg aac aac ctc ggc ggc tgc aac ggc agc acc ggc ccc agc 336
 Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110

 agt gtc aac cca gcc acc ggt aaa ccc tat ggc gcc gag ttc ccg gta 384
 Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val
 115 120 125

 ttg acc gtg gaa gac tgg gtg cac agc cag gca cgg ctg gcc gac cgc 432
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
 130 135 140

 ctg ggc atc cag cag tgg gca gct atc gtc ggc ggt agc ctg ggt ggc 480
 Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly
 145 150 155 160

 atg cag gcg ctg caa tgg acg atg acc tac ccc gag cgc gta cgc cac 528
 Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His
 165 170 175

 tgc gtc gac att gcc tcg gcc ccc aag ctg tcg gcg cag aac atc gcc 576
 Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190

 ctc aac gag gtg gcg cgt cag gcc att ctt acc gac cct gag tac cgc 624
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg
 195 200 205

 aga ggc tcg ttt cca gga cca ggt gtg atc ccc aag cgc ggc ctg atg 672

Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met						
210	215	220				
ctg gca cgg atg gtc ggc cac att acc tat ctg tcc gat gat tcg atg						720
Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met						
225	230	235				240
ggt gaa aaa ttc ggc cga gag ctg aaa gcg aca agc tca act acg act						768
Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr						
245	250	255				
tcc aca gcg tcg agt tcc agg tcg aaa gct acc tgc gct atc agg gcg						816
Ser Thr Ala Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala						
260	265	270				
agg agt ttt ccg gcc gtt tcg acg cca aca cct acc ttg atg acc aag						864
Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys						
275	280	285				
gca ctg gac tat ttc gac ccg gcc gac acg cac ggt ggt gat ctg gcc						912
Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala						
290	295	300				
gcc acc ctg gcc cac gtc acg gcg gac tac tgc atc tgt cgt tca cca						960
Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro						
305	310	315				320
ccg act gcg ctt ctc tcc ggc ccg ttc gcg cga gat cgt cga cgc gct						1008
Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Arg Ala						
325	330	335				
gat ggc cgc gcg caa gaa cgt ctg cta cct gga gat cga ttc gcc cta						1056
Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu						
340	345	350				
cgg gca cga tgc att tcc tga						1077
Arg Ala Arg Cys Ile Ser						
355						

<210> 46
<211> 358
<212> PRT
<213> *Pseudomonas putida*

<400> 46						
Met Ser Thr Val Phe Pro Glu Asp Ser Val Gly Leu Val Val Arg Gln						
1	5	10				15
Thr Ser Arg Phe Asp Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu						
20	25	30				
Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser						
35	40	45				
Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His						
50	55	60				
Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp						
65	70	75				80
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val						
85	90	95				
Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser						
100	105	110				

Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val
 115 120 125
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
 130 135 140
 Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly
 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His
 165 170 175
 Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg
 195 200 205
 Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met
 210 215 220
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr
 245 250 255
 Ser Thr Ala Ser Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala
 260 265 270
 Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys
 275 280 285
 Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala
 290 295 300
 Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro
 305 310 315 320
 Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Arg Ala
 325 330 335
 Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu
 340 345 350
 Arg Ala Arg Cys Ile Ser
 355

<210> 47
 <211> 52
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 47
 cccgggatcc gctagcgccgcg cggccggccgg cccgggtgtga aataccgcac ag 52

<210> 48
 <211> 53
 <212> DNA
 <213> Artificial sequence
 <220>

<223> Description of the artificial sequence:PCR primer

<400> 48

tctagactcg agcggccgca gccggccttt aaattgaaga cgaaagggcc tcg

53

<210> 49

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 49

gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcgga

47

<210> 50

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 50

gagaggcgcg ccgctagcgt gggcgaagaa ctccagca

38

<210> 51

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 51

gagagggcgg ccgcgcaaag tcccgcttcg tgaa

34

<210> 52

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 52

gagagggcgg ccgctcaagt cggtaagcc acgc

34

<210> 53

<211> 140

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 53

tcgaatttaa atctcgagag gcctgacgta gggcccgta ccacgcgtca tatgactagt 60

tcggacctag ggatatcgta gacatcgatg ctcttctcg ttaattaaca attggatcc 120

tctagaccccg ggatttaaat 140

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<210> 54
<211> 140
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 54
gatcatttaa atcccgggtc tagaggatcc caattgttaa ttaacgcaga agagcatcga 60
tgtcgacgt atcccttaggt ccgaactagt catatgacgc gtggtaccgg gccccacgtc 120
aggcctctcg agatttaaat 140

<210> 55
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 55
gagagcggcc gccgatcctt tttaacccat cac 33

<210> 56
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 56
aggagcggcc gccatcgca ttttcttttg cg 32

<210> 57
<211> 5091
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:plasmid

<400> 57
gccgcgactg ctttcgcgaa gccttgcccc gcggaaattt cctccaccga gttcgtgcac 60
acccttatgc caagcttctt tcaccctaaa ttcgagagat tggattctta ccgtggaaat 120
tcttcgaaa aatcgcccc tgatcgccct tgcgacgttgc gctgtcggtgc cgctgggtgc 180
gcttggcttgc accgacttgc tcagcggccg ctcgatttaa atctcgagag gcctgacgtc 240
gggccccgttgc ccacgcgtca tatgactgt tcggaccttag ggatatcgac gacatcgatg 300
ctcttcgtcg ttaattaaca attggatcc tctagacccg gatattaaat cgctagcggg 360
ctgctaaagg aagcgaaaca cgtagaaagg cagtcgcag aaacgggtgc gacccggat 420
gaatgtcagc tactggcttca tctggacaag ggaaaacgca agcgc当地 aaaaaggcaggt 480
agcttcgtcgttgc gggcttacat ggcgatagct agactggcg gttttatgga cagcaaggcga 540
accgaaattt ccagctgggg cgccctctgg taaggttggg aagccctgc aagtaaactg 600
gatggcttc ttggcccaa ggatctgtat ggcgcaggcca tcaagatctg atcaagagac 660
aggatgagga tcgtttcgca tgattgaaca agatggattt caccgcgggtt ctccggccgc 720
ttgggtggag aggctattcg gctatgtactt ggcacacacg acaatcgct gctctgtatgc 780
cgccgttgc cggctgtcag cgcaggggcg cccgggttctt tttgtcaaga ccgacactgtc 840
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<213> Artificial sequence

<220>
<223> Description of the artificial sequence:plasmid

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<210> 59
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<220>
 <223> Description of the artificial sequence:PCR Primer

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<210> 60
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 <212> DNA
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<220>
 <223> Description of the artificial sequence:PCR Primer

<400> 60
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<210> 61
 <211> 5860
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:plasmid

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<210> 62
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR Primer

<400> 62
cggcaccacc gacatcatct tcacctgccc tcgttccg 38

<210> 63
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR Primer

<400> 63		
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<210> 64		
<211> 1266		
<212> DNA		
<213> LysC mutant		
<220>		
<221> CDS		
<222> (1)..(1266)		
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Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala		
1 5 10 15		
gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct		96
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala		
20 25 30		
gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat		144
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp		
35 40 45		
gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt		192
Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg		
50 55 60		
gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc		240
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu		
65 70 75 80		
gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg		288
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr		
85 90 95		
ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc		336
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg		
100 105 110		
att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc		384
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly		
115 120 125		
aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc		432
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg		
130 135 140		
gat gtc acc acg ttg ggt cgt ggt tct gac acc act gca gtt gcg		480
Asp Val Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala		
145 150 155 160		
ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt		528
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val		
165 170 175		
gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag		576
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys		
180 185 190		
ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc		624
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly		
195 200 205		

tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn 210 215 220	672
gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu 225 230 235 240	720
att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr 245 250 255	768
ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile 260 265 270	816
tcc gat aag cca ggc gag gct gcg aag gtt ttc cgt gcg ttg gct gat Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp 275 280 285	864
gca gaa atc aac att gac atg gtt ctg cag aac gtc tct tct gta gaa Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu 290 295 300	912
gac ggc acc acc gac atc atc ttc acc tgc cct cgt tcc gac ggc cgc Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg 305 310 315 320	960
cgc gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr 325 330 335	1008
aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala 340 345 350	1056
ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu 355 360 365	1104
cgc gat gtc aac gtg aac atc gaa ttg att tcc acc tct gag att cgt Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg 370 375 380	1152
att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala 385 390 395 400	1200
ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr 405 410 415	1248
gca ggc acc gga cgc taa Ala Gly Thr Gly Arg 420	1266

<210> 65
<211> 421
<212> PRT
<213> LysC mutant

<400> 65

Val Ala Leu Val Val Gln Lys Tyr Gly Ser Ser Leu Glu Ser Ala
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Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30

Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Ileu Gln Val Gln Gly Asn Trp Thr
 325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415

Ala Gly Thr Gly Arg
 420

<210> 66
<211> 5860
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:plasmid

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<210> 67
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 67
gagactcgag gttggctggc catcatagg 29

<210> 68
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 68
gaagagagca tatgtcagcg ctctagtttgcgtt 34

<210> 69
 <211> 6472
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: plasmid

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tcccgcgca caccgcstat ggaatcgccg tcgcattgct tcacgcaaac aacagtccac	180
cggtagacgt cgacaagccc ccaaacgatc aagccaccct caaacggcgg aatttagcca	240
acaacaatag actagacaga gctgtccatg tagcatgaac tcgattatca actgccacga	300
gaggtcgggg tcatgctcac caccacaggg acgctcacgc accaaaaaat cggagacttt	360
tacaccgaag ccggagcgac gcttcacgac gtaaccatcg cctaccaagc atggggccac	420
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